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AX100704 Sequence
AJ21917 Triticum
AX100712 Sequence
AX100714 Sequence
AX100710 Sequence
AX100716 Sequence
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U39059 Lycoperation
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U39059 Homo sapi
BC028028 Homo sapi
BC015791 Homo sapi
                                                                            February 6, 2005, 17:12:26; Search time 5147 Seconds (without alignments) 10252.133 Million cell updates/sec
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BC059794 Danio rer
BC048022 Xenopus 1
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                                                                                                                                   Description
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                    4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                  OM nucleic - nucleic search, using sw model
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BC038365
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SLU39059
BC028028
CR628367
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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GGCGGTAATGCGGTCCAAAGGAAGGGGCTGTTGACCCGGATAAAGATAGGAAGGA	AGGAAGGGGCT                  AGGAAGGGGGCT	SCGGTCCAA		Qy 125 Db 125	
DB 6; Length 1089; 0; hes 0; Indels 0; Gaps 0;	Score 965; D; Pred. No. 0; 0; Mismatches	88.6%; 100.0%; rative	n Similarity 100 55; Conservative	Query Match Best Local S Matches 965	
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ez-Parra, E.C. of 01; NES CIENTIFICAS (ES)	Armenta,C.C. and Ramirez-P proteins and uses thereof 0 0121644-A 1 29-MAR-2001; UPERIOR DE INVESTIGACIONES Location/Qualifiers	z-Armenta, C. proteins ar WO 0121644-P SUPERIOR DE Location/Qu	Gutierrez-Armenta, C.C. and Wheat dp proteins and uses Patent: WO 0121644-A 1 29-N CONSEJO SUPERTOR DE INVESTI LOCATION DE INVESTI	REFERENCE 1 AUTHORS TITLE W JOURNAL E FEATURES	
Streptophyta, Embryophyta, Tracheophyta, ta, Liliopsida, Poales, Poaceae, cum.	ntae; liophy Triti	monococcum monococcum , Viridiplantae, hyta, Magnolioph Triticeae, Trit	riticum m riticum m ukaryota; permatoph ooideae;	Σ	
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ACO 7423 or none sapi BCO08075 Homo sapi AY051822 Drosophil BCO13308 Mus muscu BCO67323 Xenopus t BCO33303 Mus muscu	AY0518 AY0518 BC021 BC0673 BC033	2021 9 2528 3 2673 10 2727 5 2859 10	555 55 55 55 55 55 55 55 55 55 55 55 55	) W W 4 4 4 - 80 0 0 4 W	
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BX293986 Mouse DNA AC128086 Rattus no AC123687 Mus muscu AC110537 Mus muscu	AC128086 AC128086 AC123687 AC110537		88888 4444		

Enkarocam Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeam.

Ramirez-Parra, E. and Gutierrez, C. Characterization of wheat DP, a heterodimerization partner of th plant E2F transcription factor which stimulates E2F-DNA binding FEBS Lett. 486 (1), 73-78 (2000)

de

Direct Submission Submitted (03-FEB-2000) Gutierrez C., C.S.I.C.-U.A.M., Centro Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN Location/Qualifiers

2 (bases 1 to 1083) Gutierrez, C.

11108846

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source

dimerization partner"

function="cell cycle B2F

/gene="dp" /gene="dp" /gene="dp"

5'UTR

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ORGANISM
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PLN 16-DEC-2000

linear

mRNA 1 (dp gene).

TSP271917 1083 bp Triticum sp. mRNA for DP protein ( AJZ11917 GI:11877790 DP gene; E2F dimerization partner. Triticum sp.

RESULT 2 TSP271917 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C.
Wheat dp proteins and uses thereof
Patent: WO 0121644-A 11 29-MAR-2001,
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
Location/Qualifiers
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Wheat dp proteins and uses thereof
Patent: WO 0121644-A 7 29-WAR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
Location/Qualifiers
                   GGCCTTTCAAATTACAGATATGAAAAAAATAAAGAAGCTTGA
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Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 168; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum monococcum"
/mol_type="unassigned DNA"
/db_xref="taxon:4568"
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/note="unnamed protein product"
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/boxref="G01:13619661"
/translation="MAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSN
YRYEKIKKLEEV"
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Triticum monococcum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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                                                       CAGTTTGATGATGATCTCCCAAAACATCAAGTTACGTAACCAAAACACTGGAAAGCTCAGCAGAG
                                                                                                                            CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA
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                                  CAGTITGATGATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAG
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Gutierrez-Armenta,C.C. and Ramirez-Parra,E.C.
Gutierrez-Armenta and uses thereof
Patent: WO 0121644-A 9 29-MAR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
Location/Qualifiers
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15.4%; Score 168; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 168; Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
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Sequence 9 from Patent WO0121644.
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/db_xref="G1:1361965"
/translation="ARAAMAPPRGGAAAATAALDLTGVHILEASSVPPLPERGGNAV
ORKGAVDP
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Triticum monococcum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Triticum.
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
[ (bases 1 to 113.)
[ Gillaspy, G.E., Keddie, J.S., Oda, K. and Gruissem, W.
Plant inositol monophosphatase is a lithium-sensitive enzyme
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Gillaspy,G.E., Keddie,J.S., Oda,K. and Gruissem,W.
Direct Submission
Submission
Submitted (20-OCT-1995) Glenda E. Gillaspy, Plant Biology,
University of California, 111 Koshland Hall, Berkeley, CA 94720,
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Gutierrez-Armenta,C.C. and Ramirez-Parra,E.C.
Musat dp proteins and uses thereof
Patent: WO 0121644-A 5 29-MAR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
Location/Qualifiers
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/organism="Triticum monococcum"
/mol_type="unassigned DNA"
/db_xref="taxon:4568"
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/note="unnamed protein product"
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                                                                                                                           DNA
ATAGGAAGAGCTGGCCGCGCCACCCTTCAC 150
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Plant Cell 7 (12), 2175-2185 (1995)
                                                                                                                   Sequence 5 from Patent WO0121644.
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/db_xref="G1:13619659"
/translation="DKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADE
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                                                                                                                                                                                                                                                                                                                              164 GATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGC 223
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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Pred. No. 6.4e-71;
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/note="unnamed protein product"
/codon_start=1
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/mol_type="unassigned DNA"
/db_xref="taxon:4568"
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  organism="Triticum monococcum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 GITGCAGACGAAATITATICAGAGCTGAAGTCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GTTGCAGACGAAATTTATTCAGAGCTGAAGTCC 153
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                                                                                                                                                                                                                                14.0%; Scor.
100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX100716 150 bp
Sequence 13 from Patent WO0121644.
AX100716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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Triticum monococcum
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                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 153; Conservative
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Best Local Similarity 100.
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 224
                                                                                                                                                                                                                                                 Query Match
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ACCESSION
VERSION
KEYWORDS
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AUTHORS
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AX100716
LOCUS
                                                           CDS
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                                                                                                                                                                                                        DRIGIN
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gene="STXBP3"
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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Rlausher, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Aramenoi, R.D., Mullahy, S.J., Bodask, S.A., McZwant, P.L.,
McKernan, K.J., Malek, J.A., Qunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Gchen, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1630 bp mRNA linear PRI 30-SEP-2003
Homo sapiens syntaxin binding protein 3, mRNA (cDNA clone
IMAGE:5219755), partial cds.
                                                                                                                                                                                                                                                                                                                      FPFVCVSIGITIEKKPTVGVVYNPIIDELFTGIDGKGAFLNGKRIKVSSQSELVKALL.
ATEAGTNRDKLVVDATTGRINSLLFKVRSLRMGGSCALNLCGVACGRLDLFYELEFGG
PWDVAGGAVIVKEAGGFVFDPSGSEFDLTARRVAATNAHLKDAFIKALNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tränslation="MAQNGSVEQFLDVAVEAAKKAGE1IREGFYKTKHVBHKGMVDLV
TETDKACEDF1FNHLKQRFPSHKFIGEETTAACGNFELTDEPTWIVDPLDGTTNFVHG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1630)

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Submitted (108-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%; Score 60; DB 8; Length 1132;
100.0%; Pred. No. 8.8e-21;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                    /product="myo-inositol monophosphatase 3"
/protein id="AAB19031.1"
/db_xref="GI:1098971"
                                                                 organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                       /mol_type="mkNA"
/strain="VFNT Cherry"
                                                                                                                                     db_xref="taxon:4081"
                        Location/Qualifiers
                                                                                                                                                             13. ... 819
/codon_start=1
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Matches 60; Conservative
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USA
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BC028028
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SOURCE
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COMMENT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.maryland.sc.nih.gov/
Contact: nisc.maryland.sc.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Karline, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, K., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, E.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Mus musculus chromosome X clone RP23-75B12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 62 Row: k Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6005885.
Location/Qualifiers
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24603)
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Submitted (27-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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HTG; HTGS PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'translation="VGWEWKVVAAAPQCGEDGAAGGREGAKERRVAE"
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100.0%; Pred. No. 3e-20;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue type="Blood, adult leukocytes"
clone lib="NIH MGC_118"
lab host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="STXBP3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAH28028.1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Straubberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.D., Mullahy, S.J., Bosak, S.A., McKann, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 12 Row: k Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7656933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (105-FBB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
On Oct 28, 2003 this sequence version replaced gi:12803818.
Contact: MGC help desk
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/clone lib="NIH MGC 44"
/lab host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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db_xref="taxon:9606"
clone="MGC:3384 IMAGE:3633279"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
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/gene="C11orf10"
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JOURNAL
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                                             REFERENCE
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                                                                                                       shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC002750 444 bp mRNA linear PRI 29-JUN-2004 Homo sapiens chromosome 11 open reading frame 10, mRNA (cDNA clone MGC:3384 IMAGE:3633279), complete cds.
      humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 28, 2004 this sequence version replaced gi:51966191.
Sequence from the Mouse Genome Sequencing Consortium whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 245844 bases at least Q40
Consensus quality: 245944 bases at least Q30
Consensus quality: 245977 bases at least Q20
Insert size: 245993; sum-of-contigs
Insert size: 20507; 3.1% error; agarose-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality
coverage: 12.01x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently considers of 2 conties. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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100.0%; Pred. No. 2.9e-19;
tive 0; Mismatches 0; Indels
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1. .132816
/note="assembly_fragment:04407
fragment_chain:"
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fragment_chain:1
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                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="X"
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INV 16-JUN-2002

Query Match

Matches

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 12 BC015791

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REFERENCE AUTHORS JOURNAL

REMARK COMMENT

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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to canaferior.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /t-ānslation="MLDVVGDELKARRKHILNDIENNVKWASNRMKRQLGITSGPVKL
AASBRTARKKKERNILJGLANEENPRHAYAYABLINGIRVMAKGNESRERGAADOEV
LDVDCEMKGSABLINKRQDVVGRETEKPEPTSSFKKLADLIPVGSRTLRSLKRSSPK
APAEESFTNRSIGGFQLDYHKIFDVPLPLVEPMPEDEVMDLEDKQPVIERFCIDALG
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DEQIESLLKEALRVLRGNRQYVLATLSNAHKMPVLLDWVADRYGKSYCRAGMKSIVKT
SFRIYEKVYEKERRNKRNMLELKRSVTGLGSSISYASHKKFMSQVVQRKAEYNNKLNE
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Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Indels
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Drosophila melanogaster AT17414 full insert CDNA.
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|db_xref="GI:21429748"
|db_xref="FLYBASE:FBgn0032176"
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Lawrence Berkeley National Laboratory
Berkeley, CA 94720
0; Mismatches
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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/db_xref="taxon:7227"
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56, Conservative
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AY118692
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                                                                                                               /trānslation="MELEAMSRYTSPVNPAVFPHLTVVLLAIGMFFTAWFFVYEVTST
KYTRDIYKELLISLVASLFMGFGVLFLLLWVGIYV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: j Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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open reading frame 10"
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                                                                                                                                                                                                                                       Length 444;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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/lab host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                   1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1980 bp mRNA
Homo sapiens, clone IMAGE:4866083, mRNA.
BC015791
                                                                                                                                                                                                                                    5.1%; Score 56; DB 9;
100.0%; Pred. No. 1.3e-1
:ive 0; Mismatches
                     /protein_id="AAH02750.1"
/db_xref="G1:12803819"
/db_xref="LocusID:746"
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1. .1980
/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC015791.1 GI:16041805
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                                                                                                                                                                                                                                                                                              56; Conservative
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Best Local Similarity
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ORIGIN

FEATURES

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Vector:

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R. Siteal:

Drail! (CACCATGTO)

R. Siteal:

Drail! (CACCATGTO)

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Drail! (CACCATGTO)

R. Siteal:

Day of CACCATGTO

Description: lst strand cDNA was primed with an oligo(dT) primer

[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized

using specific. s' and 3' primers and amplified by PCR. The PCR

product was digested with Sili and size selection was performed to

exclude fragments <1.5kb.The Sili-digested PCR product was performed to

into distinct Drail! sites of pME18S-FLJ. XhoI sites just outside

the Drail! sites can be used to isolate the cDNA insert. Libraries

were constructed by oligo-capping method

(Sugano et al.,University of Tokyo, Institute of Medical Science).

Custom primer [CTTCTCTCTCTAAAGCTGCG];

3' end primer [CTTCTCTCTCTAAAGCTGC];

3' end primer [CTTCTCTCTCTAAAGCTGC];
                                                                                                                                                                                                                                                                                                                                                                                AB072761 2084 bp mRNA linear PRI 11-OCT-2001 Macaca fascicularis testis cDNA clone:QtsA-19758, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Terao,K. and Sugano,S.
Isolation of novel full-length cDNA clones from macaque testis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases I to 2084)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (09-0CT-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Irel:81-3-5285-1181) (ex.2120), Fax:81-3-5285-1181)
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Riyfrstttrlikhekknialylgkqvffttdnfetslipftifssmqvgvpevtsa
Hftgslillvvnhkvytydyesnsmnislgikhpvthvsgdnccytgslfcvdvsniv
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                         /tissue type="testis"
/clone_lib="macaque testis cDNA library QtsA"
/dev_stage="adult"
                                                                                  Length 1985;
                                                                                                                                      0; Indels
                                                                             5.1%; Score 56; DB 3; Le
100.0%; Pred. No. 1.2e-18;
ive 0; Mismatches 0;
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B072761.1 GI:16041125
oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
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/protein_id="BAB69730.1"
/db_xref="G1:16041126"
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/db_xref="taxon:9541"
/clone="QtsA-19758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca fascicularis
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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                                                                       Query Match
Best Local Simil
Matches 56; C
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AUTHORS
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JOURNAL
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                      ORIGIN
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Lorder 1. (Dates 1.0. Feingold, E.A., Grouse, L.H., Derge, J.G., Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausher, R.D., Collins, F.S., Wagner, L., Schaefer, C.K., Bhat, N. K., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.K., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K.D., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J. B., Schein, J. B., Schein, J. B., Mannerd, A., Schein, J. B., Schein, J. B., M., Schein, J. B., Schein, J. B., Mannerd, A., Schein, J. B., Schein
                                                                                                                      CSKGVLDALALQDNYSFIIEKEFYDPGFQGRQSSKDLHIVFYSYQQLGCPLLVYYDTPW
KPVVELWKCDRFQEVDAEVYLLEVNGQFSYSYSLTAKSAMCTSQPQNWTTMIKESGG
PFWNEINYSCHDPNUDABLRWPDVQYQILGGRTANQIVFSHNNGFYVFYISIVDPY
YSYCQLETVFSIYVYGAFPVQLVSAGVVWYLLISSILGSVWLAYMIPRLLRTARGRRM
TSFVAQLYGRCKTVCQFRASATARTGSKPMGRHRSS"
FAYFRGDQISQTYIYYSNTGGFSFWKYHYDRQAEIVGSLGGIFHLFSLSQVGMLVVDQ
GKGMFKYSDHPLNRSLGLSFDYNGTLDIVIATFYESGYTSDGNTKYKLDIYLKQQQHW
GRTDFNFTSSLKRATMSTLTVDIANKEISCVDIKPLSTLISVGCDLDKKIVIENTVSA
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Homo sapiens KIAA0602 protein, mRNA (cDNA clone IMAGE:5732786),
partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3430)
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Submitted (12-Jan 2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Web site: http://www.nisc.nih.gov/
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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BC065220
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 139 Row: i Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KARTILGYKTLAAGSISMAEVUPPEGGVETDLAALFESLÖYPFLIKKEGKKLOIMLORRKKY
KARTILGYKTLAAGSISMAEVUPPEGGVETDLAALFESLÖYPFLIKKEGKKLOIMLORRKKY
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FEHTSLGGROEDSDSVLSTPRKPKLFKYVSDEVLDSEODPAEHTPEAEBLDLLIYDTLDH
FRYTSLOIN PSTRASEGROAGRRERSTSIKEROPARSOMERANSLDNERCPDARSOLOIF
RYTYDSLIY PSTRASEGROAGRRERSTSIKEROPARSOMERANSLDNERCPDARSOLOIF
RYTYKTSLIY PSTRASEGROAGRRERSTSIKEROPARSOMERANSLDNERCPDARSOLOIF
RYTYSLOIN HILISDDQLPENIILVNYTSDWOGQPLSDVLORHTLPVVCTCSPADVQAA
FSTIVSRIQYRYKTSVNYNPFODLAMRDLFWKLEAGARVTREDMLGYMRFL
VIPLGSHPVARYLGSVYRYNNFFODLAMRDLFWKLEAGASAVODTPDIVSRITOYIAG
ANCAHOLPIABAMLIYKOKSPDEESSOKFIPPVGVVKVGIVEPSSATSGDSDDAAPSG
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RKRDAEKKDLPVTKNTLKCTPRSLQVSRLPSSGEAAATPTMSMTVVTKEKNKKVMFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKAKDKDVESKSQCIEGISRLICTARQQQNMLRVLIDGVECSDVKFFQLAAQWSSHVK
HFPICIFGHSKATF"
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Madro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, K., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 3430

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/mol_type="mkNa"

/db_xref="taxon:9606"

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/clone="myAGE="Brain, hippocampus"

/clone lib="NIH MGC_124"
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/db_xref="LocusID:23241"</pre>
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; 0 Query Match 5.1%; Score 56; DB 9; Length 3430; Best Local Similarity 100.0%; Pred. No. 1.2e-18; Matches 56; Conservative 0; Mismatches 0; Indels

ORIGIN

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Search completed: February 6, 2005, 20:16:32 Job time : 5152 secs

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941
1106
11196
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ORGANISM: Homo sapiens
US-09-621-976-13903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
GRGANISM: Homo sapiens
US-09-311-021-191
 US-09-621-976-13903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 191, App
Sequence 13903, A
Sequence 1, Appli
                                                                                                                                             (without alignments)
7884.537 Million cell updates/sec
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                                                                                                                                                                                                                                     Description
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                                                                                                                        February 6, 2005, 15:46:16; Search time 226 Seconds
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                 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-431-826B-465
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US-09-59-75A-465
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US-09-571-67-13081
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-09-621-976-19144
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US-09-521-976-13903

US-09-322-409-25

US-09-451-527-27

US-09-451-527-27

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                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
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Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:*
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1089
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1023
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12810
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Match Length
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Perfect score:
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No.
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Sequence 191, Application US/09311021

Patent No. 6706869

GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Pechtel, Kim
APPLICANT: Applicant Clark, Hilary
APPLICANT: Applicant Genetics Institute, Inc.
TITLE OF INVENTION: BEREFEED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6300-11A
CURRENT FILING DATE: 1999-05-13

NUMBER OF SEQ ID NOS: 268

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 191

SEQ ID NO 191
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Sequence 4, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 110, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 110, Appl
Sequence 110, Appl
Sequence 110, Appl
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Sequence 6, Appli
Sequence 6, Appli
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET, 054 PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 13903
LENGTH: 176
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1.2e-13;
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US-08-157-101A-4
US-09-149-476-310
US-09-149-476-186
US-09-149-476-186
US-08-960-022-17
US-09-68-096-11
US-09-68-096-11
US-09-668-096-11
US-09-668-096-11
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100.0%; Pred. No. 1.-.
0; Mismatches
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US-10-385-072-6
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; Patent No. 6639063
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Best Local Similarity 100.
Matches 55; Conservative
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TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (74)..(901)
US-09-322-409-25
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US-09-322-409-27/c
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Sequence 25, Application US/09322409

Sequence 25, Application US/09322409

Patent No. 6471957

Patent No. 6471957

PAPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin

APPLICANT: Preitz, Matthew J.

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C1
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Length 176;
Query Match 5.0%; Score 54; DB 4; Length 176
Best Local Similarity 100.0%; Pred. No. 3.4e-13;
Matches 54; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Zhang, Lei
APPLICANT: Yijay, Hari M.
APPLICANT: Rode, Harid M.
APPLICANT: Rode, Harid M.
APPLICANT: Rode, Harid M.
APPLICANT: Rode, Harid M.
NUMBER OF INVENTION: ALLERGEN OF CLADOSPORIUM HERBARUM NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seaby and Maclean
ADDRESSEE: Seaby and Maclean
STREET: 880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA and its encoded protein FEATURE: open reading frame of CH2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Ottawa
COUNTRY: Canada
CONDUTER: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette.
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,414E
FILING DATE: January 24, 1994
CLASSIFICATION NUMBER: US/08/185,414E
FILING DATE: JANUARY 24, 1994
CLASSIFICATION NUMBER: 24,034
REGISTRATION NUMBER: 1747
TELEPHONE: (613) 232-5815
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TELEPHONE: GLARACTERISTICS:
LENGTH: 630 base pairs
TELENGTH: 630 base pairs
TELENGTH: 630 base pairs
TELENGTH: 630 base pairs
TELENGTH: 630 base pairs
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US-08-185-414E-1
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Sequence 27, Application US/09322409

Sequence 27, Application US/09322409

Patent NO. 6471957

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Sim, Gek-Kee

APPLICANT: Wathew J.

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Patent No. 6482403
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: CANINE AND USES THEREOF
FILE REFERENCE: IM.2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT TILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 985;
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5.0%; Score 54; DB 4; -Le
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 4; Le
Pred. No. 2.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.0%; Score 54; DB Best Local Similarity 100.0%; Pred. No. 2.9 Matches 54; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PATENTIN Ver. 2.0
SOOTUN 02 25
LENGTH: 985
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SEQ ID NO 27
LENGTH: 985
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ORGANISM: Canis familiaris
US-09-322-409-27
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ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-010-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.0%; Score 54; DB 4; Loudo.0%; Pred. No. 2.9e-13; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.0%; Score 54; DB 1; L
100.0%; Pred. No. 2.9e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                      NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: PHCR17694
TELEPHONE: (206) 682-8100
TELEPHONE: (206) 224-0779
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TYPE: nucleic acid
STRANDEDNES: single
TYPE: CDNA to mRNA
DESCRIPTION: clone 20; see Figure 27
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: CONR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
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SEQ ID NO 58
LENGTH: 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 54; Conservative
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CORGANISM: Homo sapiens
US-09-482-273-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-252-966B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-482-273-58
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Matches
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Sequence 27, Application US/09451527

Patent No. 6482403

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C2

CURRENT APPLICATION NUMBER: US/09/451,527

CURRENT APPLICATION NUMBER: US/09/451,527

CURRENT APPLICATION NUMBER: US/09/322,409

EARLIER PILING DATE: 1999-12-01

EARLIER PILING DATE: 1999-05-29

MUMBER OF SEQ ID NOS: 174

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 27

LENGTH: 985
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC STREET: 1420 Fifth Ave., Suite 2800 CITY: Seattle STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Elsenman, Robert N.
APPLICANT: Hullin, Peter J.
APPLICANT: Hullin, Peter J.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
TITLE OF INVENTION: And or Max
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                    5.0%; Score 54; DB 4; Length 985;
100.0%; Pred. No. 2.9e-13;
Live 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 54; Conservative 0; Mismatches 0; Indels
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08252966B Patent No. 5624818
                                                                                                                                   TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (74)..(901)
US-09-451-527-25
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US-09-451-527-27/c
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Length 1023;

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Length 1050;

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Query Match 5.0%; Score 54; DB 4; Length 1810; Best Local Similarity 100.0%; Pred. No. 2.8e-13; Matches 54; Conservative 0; Mismatches 0; Indels
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Sequence 77, Application US/09800729

Sequence 77, Application US/09800729

PATENTE NO. 605592

TILLS OF INVENTION:

TILLS OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT PAPLICATION NUMBER: 2001-03-08

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SEQ ID NO 77

INVERTE: PatentIn Ver. 2.0
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Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
                                                                                                                  CURRENT PELLING DATE: 2001-03-08
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-24
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 1810
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: SITE

LOCATION: (1803)

OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1804)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-77
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Patent No. 6512164
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (1804)
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US-09-594-506-37
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                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-09-08
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APPLICANT: Shi, Jinrui
TITLE OF INVENTION: A No. 6720478el Maize Rad51-Like Gene and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 1107
CURRENT APPLICATION NUMBER: US/09/537,654
CURRENT APPLICATION NUMBER: 60/132,582
EARLIER APPLICATION WUMBER: 60/132,582
EARLIER FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
: LENTH: 1459
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Pred. No. 2.8e-13;
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Best Local Similarity 100.0%; Pred. No. 2.6
Matches 54; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 463
LENGTH: 1358
                                                                                           Sequence 463, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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; LOCATION: (169)...(1011)
US-09-537-654-3
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US-09-949-016-463
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US-09-800-729-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Patent No. 6657054
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFRENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT ELING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 3438
                                                                                                                                                                                                                                                                                                                        Query Match 5.0%; Score 54; DB 4; Length 2406; Best Local Similarity 100.0%; Pred. No. 2.7e-13; Matches 54; Conservative 0; Mismatches 0; Indels
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5.0%; Score 54; DB 4; Length 3438;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 54; Conservative 0; Mismatches 0; Indels
## APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Thiamine Biosynthetic Enzymes
FILE REPERENCE: BB1372 US NA
CURRENT APPLICATION NUMBER: US/09/594,506
CURRENT FILING DATE: 2000-06-15
PRIOR PILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Microsoft Office 97
SEQ ID NO 37
LENGTH: 2406
                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-594-506-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (527)..(2701)
; OTHER INFORMATION:
US-10-164-595-29
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-164-595-29
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Search completed: February 6, 2005, 17:39:37 Job time: 228 secs

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CD82264 G118.121J
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CA802821 Sau4202.
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CB371210 TGSSTZYG9
AL697897 DKFZD686A
BG179244 6C2330836
CC0249876 AGENCOURT
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CA934974
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                  - nucleic search, using sw model
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CB371210
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Maximum DB seq length: 200000000
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CV497760 61986.1 M CK085723 RG6_F02 C B1377034 BELG3 000 CD722238 0j07b10.y BG164383 602341982 CK933853 CGF100443 B1377697 BFLG3 001 C92906 C92906 Dict BB907643 601497651 CN992367 70294 L25 B1861964 601311664 BU958316 AGENCOURT BES9416 601311664 BU958316 AGENCOURT BES97000 601492711 BES29946 99AS179 R B194247 8m48E64.y CF317851 HD07-L0 AW481765 37984 MAR CK121803 201003.p1 CC168353 Mdfr2002d	ALIGNMENTS  ALIGNMENTS  1188HC library Triticum aestivum genomic clone  101:51666086  aestivum  4 Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  110:5166086  aestivum  110:5160808  aestivum  110:540  Aestaelenes  110:540  Aestaelenes  110:540  Aestaelenes  110:540  Aestaelenes  110:540  Aestaelenes  110:540  Aestaelenes  Aestaelene	
CV497760 CK085723 B1377034 CD122238 BG164383 CK938853 BE307643 CK932367 BES07643 BES07643 BES07643 BES07643 BES07643 BES07960 BES29946 BES29946 BES29946 BES29946 AM481765 CK121803 CC168353	ALIGNMENTS  ALIGNMENTS  1188HC library Triticum aee  101;5166086  aestivum (bread wheat) aestivum (bread wheat) aestivum (bread wheat) aestivum and viridiplantae; Streptophy phyta; Magnoliophyta; Liliop i Triticeae; Triticum; c.D., PeterSon, D.G., Li, W., c.D., PeterSon, D.G., Li, W., c.D., DeterSon, D.G., Li, W., coll Sandalitiers 1000  10	Score 107; Pred. No. 0; Mismatch GGGGGGAGCTGC
LL404L40UL4UUUU4LULLU	libra   libra  libra  libra  libra  libra  libra  libra  libra  libra  l	. 8 * ; . 0 · 0 * ; . 0 · 0 · 0 · 0 · 0 · 0 · 0 · 0 · 0 · 0
458 460 4999 4999 4999 6089 6089 6089 6089 6089 6089 6089 6	1188HC library 101. genomic su 1 GI:5166086 aestivum (brea aestivum i, Viridiplanta i, Viridiplanta hyta; magnolio hyta; magnolio hyta; no 694) i.D. Peterson, i.D. Sagnolio j.D. Sagnoli	Clone_11D=1   1arity
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CA802821.1 GI:26059907
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Best Local Similarity 100.
Matches 88; Conservative
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                                                                                                                   CD892664 454 bp mRNA linear EST 14-JUL-2003 G118.121J23F010725 G118 Triticum aestivum cDNA clone G118121J23, mRNA sequence.
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Triticum aestivum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
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Triticum aestivum
Triticum aestivum
Triticum aestivum
Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                        93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 56 10

pris sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="recital"
/cultivar="recital"
/clone="G118121J23"
/tissue type="grain (118 degrees per day after
pollination)"
 Query Match
9.0%; Score 98; DB 6; Length 454;
Best Local Similarity 99.3%; Pred. No. 5.9e-36;
Matches 148; Conservative 0; Mismatches 1; Indels
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CD882927.1 GI:32645392
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Mismatches

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59; Conservative
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                                                                                                                                                                               Jab hose="DH10B"

/clone_lib="Gem-c1071"

/clone_lib="Gem-c1071"

/clone_lib="Gem-c1071"

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/clone_lib="Gem-c1071"

/clone_lib="Gem-c1071"

/clone_lib="Gem-c1071"

/clone_lib="Gem-c1071"

/clonelib="Gem-c1071"

plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.

Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a NotI restrictions site. Sall
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-Sall restriction
site of the pSPORTI vector. The ligated cDNA fragments
were transformed into a cools ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinios at
Urbana-Champaign. email: l-vodkin@uiuc.edu"
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Busaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roside; euroside I; Majnoliophiales; Salicaceae; Salicacea; Populus.

[ (Dases 1 to 318)
Brosche, M. Alatalo, E. R., Vinocur, B., Altman, A., Teichmann, T.,
Ottow, E.A., Polle, A., Dillianov, D., Afif, D., Triboulot, M.B.,
Dreyer, E., Paulin, L., and Kangasjaervi, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1071-3748"
/tissue_type="immature pods (~2cm long) of greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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/note="country: China:Xinjiang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4%; Score 59; DB 6; Length 301;
100.0%; Pred. No. 4.4e-17;
live 0; Mismatches 0; Indels
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Pred. No. 4.4e-17;
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Department of Biosciences, Plant Physiology
University of Helsinki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Populus euphratica"
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/db_xref="taxon:75702"
/clone="P0000300024G01F1"
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Unpublished (2004)
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                         /organism="Glycine max"
                                               /mol_type="mRNA"
/cultivar="Williams"
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Location/Qualifiers
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100.0%;
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Matches 59; Conservative
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TGESTZYG99C09.x1 TgME49 3 day invitro bradyzoite Toxoplasma gondii CDNA clone TgESTzyg99c09.x1 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Putative full length read
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1 (bases 1 to 157)
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Hiller, L., Bennett, J., Franklin, C., Tasgareishvill, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                          Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Sarcocystidae, Toxoplasma.
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5.3%; Score 58; DB 6; Le:
Best Local.Similarity 100.0%; Pred. No. 1.4e-16;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector to vector length is
Seg primer: -40UP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Clifton,
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Homo sapiens (human)
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CO249876
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B. (bases 1 to 177)
S. Mational Institutes of Health, Mammalian Gene Collection (MGC)
Inpublished (1999)
C. Ontact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                   AL697897 1686 (synonym: hlcc3) Homo sapiens CDNA clone DKFZp686A19105_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone DKFZp686A19105_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169)

Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.

EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA" sepiens"
/mol_type="mRNA" sepiens / clone="breadus sepiens / do verse="breadus set / do verse="breadus / do verse="breadus | / lab_host="bhi0B" / clone="lb="686 (synonym: hlcc3)" / note="vector: pTriplEx2; Stre_1: SfilA; Site_2: SfilB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKT2), Email 8. Wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No 81 sequence available.

This clone (DKFZp686A19105) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.1%; Score 56; DB 1; Length 169; Best Local Similarity 100.0%; Pred. No. 1.3e-15; Matches 56; Conservative 0; Mismatches 0; Indels
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                                                                                                                 AL697897.1 GI:19618437
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SM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 214)

SNIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="adenocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/loore="lorgan: prostate; Vector: pCWV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Site_1: Shorts size 1.4 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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//mol_type="mRNA"
//db xref="texon:9606"
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//tissue_type="Chondrosarcoma Lung Metastasis cell lines"
//tissue_type="Chondrosarcoma Lung metastant"
//clone lih="Din MGC 212"
//note="Organ: Lung; Vector: pXX-Asc; Site_1: EcoR I;
//clone lih="Nul MGC 212"
//note="Organ: Lung; Vector: pXX-Asc; Site_1: BcoR I;
//clone lih="Organ: Lung; Vector: pXX-Asc; Site_
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
High quality sequence stop: 214.
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AGENCOURT 26529183 NIH_MGC_212 Homo sapiens cDNA clone
IMAGE319925067 5', mRNA sequence.
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM10188 row: g column: 10
High quality sequence start: 3
High quality sequence stop: 169.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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ORIGIN

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Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Eax: 314 286 1800
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTS on Clone' is listed in the 'Other ESTS on Clone' is listed in the 'Other ESTS on Olone' is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Putative full length read vector to vector length is 392
Seq primer: -40RP from Gibco
High quality sequence stop: 213.
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/db xref="taxton:s847"
/clone="SOYBEAN CLONE ID: Gm-c1071-2376"
/tissue type="1" mmature pods (~2cm long) of greenhouse
grown plants"
/lab host="DH10B"
/clone lib="Gm-c1071"
/note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; The
cDNA library was constructed from mRNA isolated from
immature pods (approximately 2cm long) of greenhouse grown
plants. The library was prepared using the Life
Technologies pSuperSoript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a NotI restrictions site. Sal1
gel. First strand cDNA synthesis was primed with oligo-dT primer containing a NoI I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionmally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GATAAGGCCA. Tissue was provided by Mary Hendrix."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.,
Public Soybean, EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA802105 223 bp mRNA linear EST 01-JUL-2004 sau30b12.y1 Gm-c1071 Glycine max CDNA clone SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                                                                                                                                                                                                                                                Length 214;
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                1 Similarity 100.0%; Pred. No. 1.3e-15; 56; Conservative 0; Mismatches 0;
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/cultivar="Williams"
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Best Local (
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TITLE COMMENT FEATURES

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linkers adapters were ligated to the blunt-ended cDNA fragments followed by Not1 digestion. The CDNA fragments were directionally cloned into the Not1-Sal1 restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Uvokxin by Anu Khanna at the University of Illinios at Urbana-Champaign. email: l-vodkin@uluc.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Brain; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb, Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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ip35e06.gl Brain - Cerebellum Library (DOGEST8) Canis familiaris
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                                                                                                                                                                                                                   Length 223;
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/dev stage="3 month old normal canine"
/lab_host="XLIO Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: W. Richard McCombie
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
Dex 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 262)
Balija,V., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris cerebellum (dog)
                                                                                                                                                                                                                   DB 6; Le
1.3e-15;
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100.0%; Pred. No. 1...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA clone ip35e06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mccomble@cshl.org
Plate: ip35 row: e column: 06
High quality sequence stop: 276.
Location/Qualiflers
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/db_xref="taxon:9615"
/clone="ip35e06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN005830.1 GI:45769978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (dog)
                                                                                                                                                                                                                                                            56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris
                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 56; Conserv
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LOCUS DEFINITION

ACCESSION

VERSION

RESULT 12 AW734913

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dKf2- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
AL046990 287 bp mRNA linear EST 04-SEP-2003 DKFZp586L2017_r1 586 (synonym: hutel) Homo sapiens cDNA clone DKFZp586L2017_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bi's5116 25-SEP-2001
603030013F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5200226 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 290)
                                                                                                                                                                                                                                    Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="586 (synonym: hute1)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1/Mlu1"
                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostom. Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 287)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)

On Jul 9, 1999 this sequence version replaced gi:5435046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone (DKFZD58612017) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Preparation: Life Technologies, Inc.
CDNA Library Darrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 1.3e-15; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .287
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp586L2017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="uterus"
|dev_stage="adult"
|lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No s1 sequence available.
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BI756116.1 GI:15747694
                                                                                                                               AL046990.2 GI:5936321
                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MIPS
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Than 56; Conserva
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BI756116
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="GRNOME SYSTEMS CLONE ID: Gm-c1016-10054"
/tisbue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
/clone lib="Gm-c101016"
/clone lib="Gm-c101016"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction ktr. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoNA. XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Email: estewatson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: -40RP from Gibco
High quality sequence stopp: 227.
                                                                                                                                                                                                                                                                                                                                                                                                                               J. Chaese, L. C. 20.7, Kalm, P., Vodkin, L., Erpelding, J., Coryell, V., Khama, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Schurk, R., Riter, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
                                                  sk76f11.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-10054 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
                                                                                                                                                                                  AW734913.1 GI:7640550
                                                                                                                                                                                                                                          Glycine max (soybean)
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 269)
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Best Local Similarity 100.
Matches 56; Conservative
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source

FEATURES

RESULT 13 AL046990

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Indels

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/lab_host="DH108"
/clone lib="NIH MGC 114"
/note="Corgan: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGESTOOLS Anopheles gambiae adult pSport cDNA Anopheles gambiae Adult pSport cDNA Anopheles gambiae AA413331
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/clone_lib="Anopheles gambiae adult pSport cDNA"
/note="Site_1: Sal1; Site_2: Not1; See: Salazar, C.E., et al. Insect Molecular Biology (1994), 3:1-13."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornel, A.J., Kumar, V., Mukabayire, O., Salazar Rafferty, C., Petrarca, V., Coluzzi, M. and Collins, F.H.
A comprehensive physical map of the malaria vector Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.1%; Score 56; DB 4; Length 290; Best Local Similarity 100.0%; Pred. No. 1.3e-15; Matches 56; Conservative 0; Mismatches 0; Indels
found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LibMl1501 row: j column: 03
High quality sequence stop: 236.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Other ESTs: AgEST00035
Contact: Salazar Rafferty, C.; and Collins, FH Vector Genetics Section
Centers for Disease Control and Prevention
MS F-22, 4770 Buford Hwy, Chamblee, GA 30341
Tel: 770 488 7469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: czs7@cdc.gov
Mapping location: 34C in 3R chromosome
Seq primer: M13 Universal
High quality sequence stop: 294.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Anopheles gambiae"
                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5200226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:7165"
/clone="cc38"
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/strain="G3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA413331.1 GI:2071917
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1 (bases 1 to 294)
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AA413331/c
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Search completed: February 6, 2005, 18:50:42 Job time: 4259 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 6, 2005, 14:35:16; Search time 698 Seconds (without alignments) 9235.814 Million cell updates/sec Run on:

US-10-088-830-1 1089 Title: Perfect score:

Sequence:

OLIGO NUC Gapop 60.0 , Gapext 60.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

4: geneseqn2001s:\*

5: geneseqn201as:\*

6: geneseqn201as:\*

7: geneseqn201as:\*

8: geneseqn203as:\*

9: geneseqn203as:\* geneseqn2003cs:\* geneseqn2003ds:\* genesegn2004as:\* genesegn2004bs:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

																٠				
Description	Aaf80144 Nucleotid	Aaf80149 DNA fragm	Aaf80148 DNA fragm	Aaf80147 DNA fragm	DNA	Aaf80146 DNA fragm	Aah64916 Human sec	Abv58410 Human pro	Aad02077 cDNA enco	Abx42327 Bovine ES	Aai90926 Human pol	Aaz52570 Human sec	Aac77635 Human can	Adg22529 Human sof	Aac58600 Human PRO	Aaz34292 Human PRO	Aac78580 Human PRO	Aas21446 Human cDN	Abk33602 cDNA enco	Abl88117 Human PRO
ΔI	AAF80144	AAF80149	AAF80148	AAF80147	AAF80150	AAF80146	AAH64916	ABV58410	AAD02077	ABX42327	AA190926	AAZ52570	AAC77635	ADQ22529	AAC58600	AAZ34292	AAC78580	AAS21446	ABK33602	ABL88117
08	4	4	4	4	4	4	Ŋ	ഗ	m	œ	4	m	m	12	m	~	m	4	9	9
% Query Match Length DB	1089	168	168	153	150	156	668	376	396	410	443	491	917	2435	3759	3819	3819	3819	3819	3819
& Query Match	88.6	15.4	15.4	14.0	13.8	10.5	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1
Score	965	168	168	153	150	114	26	55	52	5	52	52	55	55	52	55	55	55	52	22
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### ALIGNMENTS

E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation; Nucleotide sequence of a wheat E2F-dimerisation partner (DP) protein. AAF80144 standard; DNA; 1089 BP. 11-JUN-2001: (first entry) Triticum monococcum. AAF80144; 

Location/Qualifiers 20. .805 /\*tag= a /product= "B2F-dimerisation partner (DP) protein"

WO200121644-A2.

25-SEP-2000; 2000WO-EP009325. 29-MAR-2001.

99ES-00002127. 99ES-00002474. 24-SEP-1999; 11-NOV-1999; (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

Gutierrez-Armenta C, Ramirez-Parra E;

WPI; 2001-257972/26.

P-PSDB; AAB67762.

New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.

Claim 13; Fig 1; 77pp; English.

The present sequence encodes a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F-DP domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size 8  $\frac{1}{2}$   $\frac{1}{2}$ 

Sequence 1089 BP; 367 A; 215 C; 261 G; 246 T; 0 U; 0 Other;

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244 724 184 244 304 364 424 484 484 544 544 604 664 724 784 844 844 904 904 304 364 CAGTTTGATGATCTCCCAAAACATCAAGTTACGTAACCAAACACGCAAAGCTCAGCAGAG 604 664 784 964 964 245 GAGAAAGTIGAAGCCAAAGGAAGAACAACATACAATGAGGTIGCAGACGAAATITATITCA AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTG 725 ACATTGCATGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACACCATAGGAAGAGCT CTGGCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAACTTG ACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGATTTTAACCTGCAAATTTTGTCTC GGCGGTAATGCGGTCCAAAGGAAGGGCCTGTTGACCCGGATAAAGATAGGAAGAAGAG GGCGGTAATGCGGTCCAAAGGAGGGGCTGTTGACCCCGGATAAAGATAGGAAGAAGAG GAGAAAGTTGAAGCCCAAAGGAAGAACAACATAACAATGAGGTTGCAGACGAAATTTATTCA CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA CAGITICATOATCICCOAAACATCAAGITACGIAACCAAACACIGGAAAGCICAGAGAG GAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTCAATGGTGCACATTC CTGGCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAACTTG ACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGATTTTAACCTGCAAATTTTGTCTC AAGGCTGCGCCACCAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAATAGTTTGT AAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGCCGAGTACACAAATAGTTTGT GAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTTGATGAGAAGAATATTAGGCGGAGA AATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTG GAAATTGAGATTCAGATGACTCGAAGTTTGCCCATTTCGAGTTCAATGGTGCACCATTC GGCCGCCCCCCTCCACTAGAGACTCAAGAATATTACAAATGAATTAAAAAGTGTTAGAA ACATTGCATGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGACATAGGAAGAGCT Gaps ; DB 4; Length 1089; 0; Indels 88.6%; Score 965; DE 100.0%; Pred. No. 0; ive 0; Mismatches 88.6%; Best Local Similarity 100. Matches 965; Conservative 185 245 305 365 545 545 605 665 125 485 905 Query Match Best Local & 125 185 305 365 425 425 485 605 665 725 785 785 845 845

AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a heterodimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA blinding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, ö phase; New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size. 2P-dimerisation partner; DP protein; E2F transcription factor; G1 pha phase; cell cycle; retinoblastoma protein; alter cell proliferation; 965 CTTTTTGIGCCTAGCAGGTTATTAGGTCTCAGATAGATGATTCATATATGTGCTGCTATG 485 CGTAAAGAACTCGTCAACAATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein. Length 168; Indels Sequence 168 BP; 62 A; 38 C; 33 G; 35 T; 0 U; 0 Other; Query Match
15.4%; Score 168; DB 4; Local Similarity 100.0%; Pred. No. 1.8e-49;
Matches 168; Conservative 0; Mismatches 0; (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF. Ä Disclosure; Page 74-75; 77pp; English. Ramirez-Parra ВР 99ES-00002127. 25-SEP-2000; 2000WO-EP009325 AAF80149 standard; DNA; 168 (first entry) Gutierrez-Armenta C, organ or tissue size WPI; 2001-257972/26. P-PSDB; AAB67767. Triticum monococcum 1085 AAAAA 1089 AAAAA 1089 E2F-dimerisation WO200121644-A2 24-SEP-1999; 11-NOV-1999; 11-JUN-2001 29-MAR-2001 1025 965 AAF80149; RESULT 2 AAF80149 엄 g q 8XCCCCCCCCCCX8X444XX88X5X8X8X6X6X8X8X8X8X8X8X8X8X8 ઠ ò ð

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AAP80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblatoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblatoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size
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                                                                   61 CAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAAAACCTGGAAAGCTCAGCAGAG 120
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1 CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA 60
                                                                                                                                                                                                                                                                                                                                DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein.
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1 ATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCT 317 ATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCT

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AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a heterodimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size
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14.0%; Score 153; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 3.4e-44;
Matches 153; Conservative 0; Mismatches 0;
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13.8%; Score 150; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 150; Conservative 0; Mismatches 0; Indels
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                  121 GTTGCAGACGAAATTTATTCAGAGCTGAAGTCC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an factor. E2F and DP are two proteins that hetero-dimerise to form an earlive transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly content of the plant cell, organ or tissue shape, and particularly content of the plant cell, organ or tissue shape, and particularly contents.
                                                                                                                                                                                                                                         E2F-dimerisation partner; DP protein, E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCACGAGCCGCCATGCGCGCCTCCCCGCGGAGCTGCTGCGGCCGCTACCGCCGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                            DNA fragment encoding a wheat E2F-dimerisation partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 156 BP; 24 A; 58 C; 51 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 114; DB 4; 1
Pred. No. 1.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.5%; Score 114; DE
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 114; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 71-72; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramirez-Parra E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH64916 standard; cDNA; 668 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99ES-00002127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2000; 2000WO-EP009325
AAF80146 standard; DNA; 156
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gutierrez-Armenta C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organ or tissue size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-257972/26.
                                                                                                                                                                                                                                                                                                                                                                                          Triticum monococcum.
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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they decode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's gene expression by binding with the cells' own genes and preventing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide con the present sequence is a GENSET nucleic acid of expression and activity. The present sequence is a GENSET nucleic acid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; gene therapy; vaccine; treatment; diagnosis; GENSET; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 5; Length 668; Pred. No. 2.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 668 BP; 188 A; 163 C; 151 G; 166 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Bougueleret L, Jobert S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 58401.
                                                         Human secreted protein cDNA, SEQ ID NO: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.1%; Score 56; UB
Best Local Similarity 100.0%; Pred. No. 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 753; 921pp; English
                                                                                                                                                                                                                                                                         07-DEC-2000; 2000WO-IB001938
                                                                                                                                                                                                                                                                                                                08-DEC-1999; 99US-0169629P
06-MAR-2000; 2000US-0187470P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV58410 standard; cDNA; 376
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-367870/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAG89313
                                                                                                                                                                                             WO200142451-A2
                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                              08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2002
                  11-SEP-2001
                                                                                                                                                                                                                                  14-JUN-2001.
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ABV58410
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AC ABV5.
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DT 13-S.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate call carcinogenic optential of a composition for inhibiting prostate cancer in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat, pituitary, pituitrone, therapy, immune disorder, anaemia; Digeorge syndrome; haematopoietic cell; ataxia telangicctasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease, autoimmune disorder; multiple selrosis; systemic lupus erythematosus; SLE; hyperproliferative disorder; gene therapy; neoplasm; infectious disease; immunomodulatory; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 55; DB 5; Length 376; 000.0%; Pred. No. 6.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 376 BP; 164 A; 68 C; 61 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA encoding rat pituitary hormone, pituitrone.
                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%; Pred. No. 6.8
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1, Page 11212; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                  Schlegel R, Endege WO, Monahan JE;
pharmacogenomic marker; gene;
                                                                                                                                             20-FEB-2001; 2001WO-US005171.
                                                                                                                                                                                                  2000US-0189862P.
2000US-0207454P.
                                                                                                                                                                                                                                     09-JUN-2000; 2000US-0211314P
                                                                                                                                                                                                                                                  2000US-0219007P
                                                                                                                                                                                                                                                                         13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD02077 standard; cDNA; 396
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les 55; Conserv
                                                                      WO200160860-A2
                                    Homo sapiens.
                                                                                                                                                                                                  16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                          18-JUL-2000;
                                                                                                                                                                               17-FEB-2000;
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                                                                                                         23-AUG-2001
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Matches
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Location/Qualifiers

Rattus sp

Gaps ö Key

24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P 11-JAN-2000; 2000US-00480902

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a novel pituitary hormone (pituitrone), useful for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders.
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                          /*tag= a
/product= "Rat pituitary hormone, pituitrone"
/note= "Does not include start codon"
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100.0%; Pred. No. 6.7e-10;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 396 BP; 110 A; 135 C; 91 G; 60 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 269; 277pp; English.
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                                                                                                                                                                                                                                                                                                                27-APR-2000; 2000WO-US011211.
                                                                                                                                                                                                                                                                                                                                                                           99US-0131966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55; Conservative
                                                                                                                     /partial
. . 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-687547/67.
P-PSDB; AAY71961.
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                                                                                                                                                                                    WO200066778-A1
                                                                                                                                                                                                                                                                                                                                                                           30-APR-1999;
                                                                                                                                                                                                                                               09-NOV-2000
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ABX42327/c
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CDS
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The invention relates to a purified nucleic acid molecule associated with

Claim 2; SEQ ID NO 7492; 245pp; English

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Warren WC;

Tao N,

Byatt JC, Mathialagan N,

(WARR/) WARREN W C.

TAON/)

WPI; 2003-110599/10.

(BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.

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lactuation relates to a purilled nucleic acid molecule associated with cattle, and the LMFD nucleic acid can specifically hybridise to a second cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (11) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonuclecides to a 3' end of the mRNA molecule; and of polyadenylated ribonuclecides to a wolecule in a bovine cell or tissue comprising; all incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is predictive of the certification of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The PMFD nucleic acid acide 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nnetically improving cattle. The present sequence is one of the bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The t sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html?DocID=20020137139
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Best Local Similarity
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Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

US2002137139-A1

Bos Taurus

26-SEP-2002

Bovine EST associated with lactation/muscle/fat deposition #7492.

(first entry)

20-FEB-2003

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polymucleotides obtained from adult testes, foetal brain, adult brain, brain (foetal and adult), foetal kidney, adult spleen, and adult thymus brain (foetal and adult), foetal kidney, adult spleen, and adult thymus constant libraries. The polymucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haematopoiesis regulating activity, considerations activity, chemotactic/chemokineit activity, haematopoiesis regulating activity, consolication activity, and thromostatic and thromoblytic activity, and tumnour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Therapeutic compositions are also presently valuable for veterinary applications. AAZ5281 encode human secreted proteins, and AAX73390 to AAX73500 represent human secreted proteins, given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, cancer associated gene, cancer antigen; detection, cancer, diagnosis; cytostatic; proliferative, vulnerary, immunomodulator; antidathmatic; antirhematic; antiarhritic; antiarhritic; antidathitic; antidathitic; antidation; antidiffammatory, antithyroid; antidallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides and proteins having biological activities which make them suitable for treating, preventing or ameliorating medical conditions in humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes human secreted proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 491 BP; 133 A; 148 C; 114 G; 96 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer associated gene sequence SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%; Score 55; DB 3; Le
100.0%; Pred. No. 6.4e-10;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  Clark HF, Fechtel K, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 200; Page 702; 730pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC77635 standard; cDNA; 917 BP
                      98US-0099950P.
98US-0100424P.
98US-0103329P.
98US-0103615P.
98US-0111799P.
                                                                                                                                                             98US-0114415P.
99US-00248059.
99US-00287150.
  98US-0099843P
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                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-053095/04.
P-PSDB; AAY73485.
                                                                                                                                                                                                                                    13-MAY-1999;
                           11-SEP-1998
                                                                         29-SEP-1998
                                                                                                                 11-DEC-1998
14-DEC-1998
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                                                                                                                                                                                                                                                                                                                                  Wong GG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polymucleotides (AAI79941-AAI91841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or readment of cancer, laukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein clone yd261_1 nucleotide sequence SEQ ID NO:191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; immunostimulatory; haemostatic; cytokine;
proliferative; differentiative; chemotactic; chemokinetic; vaccine;
thrombolytic; antiinflammatory; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 10986; 1399pp + Sequence Listing; English.
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100.0%; Pred. No. 6.5e-10;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 443 BP; 183 A; 68 C; 96 G; 96 T; 0 U; 0 Other;
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                                                                                                                                    26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                 28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US010843
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                                                                                                                                                                                                                                                                                                                                                   2001-514838/56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAO10995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; ss.
                                       WO200164835-A2
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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17-AUG-1998;
                                                                                        07-SEP-2001
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Matches

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RESULT 12
AA252570
ID AA252
XX
AC AA252
XX
XX
DT 29-FE
XX
DT 29-FE
XX
HUMAN
XX
HUMAN
XX
HUMAN
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HOMO
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HOMO
XX
YX
PD 18-NO
XX
YX
PD 18-NO
XX
PF 14-MA
PR 17-AM

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0; Indels

Length 491;

10-JUN-2004

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ARB4339 to AAB44339. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antidathetic; antidathetic; antidathetic; antidathetic; antidathetic; antidathetic; antidathetic; antidathetic; coagulator; chermatological; neuroprotective; caddiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antidanglogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, uncommune calsorders in the totract disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC77607 to AAC78448 encode the human cancer associated proteins given in
                                                                                                                                                                                                                                                                                                                                                                                       isolated nucleic acids comprising sequences encoding peptides 1 for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 917 BP; 247 A; 269 C; 257 G; 142 T; 0 U; 2 Other;
neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 632; 2352pp; English
                                                                                                                                                             08-MAR-2000; 2000WO-US005882
                                                                                                                                                                                                     99US-0124270P
                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention
                                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                            WPI; 2000-587533/55
                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB43426
                                                                              WO200055350-A1.
                                                                                                                                                                                                   12-MAR-1999;
                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                          useful
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0
Score 55; DB 3; Length 917; Pred. No. 5.5e-10;
                0; Indels
    100.0%; Pred. av.
                55; Conservative
         Best Local Similarity
Query Match
                Matches
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soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                  Human soft tissue sarcoma-upregulated DNA - SEQ ID 5349.
ADQ22529 Btandard; DNA; 2435 BP
                                             (first entry)
                                          26-AUG-2004
                                                                                                                          Homo sapiens
                      ADQ22529;
BX SX M X E X E X S X S X I
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WO2004048938-A2

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both same or different individual, of protein expression in the first soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated bnA of the invention. The current sequence is not shown within the
                                                                                                                                                                                                                                                                             Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective; antianteanci; hepatotropic; virucide; antipsoriatic; antiallergic; antiantacic; systemic luque erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolyvic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelliating disease; hepatobliary disease; Mhipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immune-mediated skin disease; allergic disease; inflammatory disease; transplantation associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO1083 protein UNQ540 encoding cDNA SEQ ID NO:116.
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5.1%; Score 55; DB
Best Local Similarity 100.0%; Pred. No. 4.4
Matches 55; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 5349; 210pp; English.
                                                                                                                                                                                          Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC58600 standard; cDNA; 3759 BP.
                                                                                                                                                  (PROT-) PROTEIN DESIGN LABS INC.
                                                              26-NOV-2003; 2003WO-US038193.
                                                                                                         2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2001 (first entry)
                                                                                                                                                                                            Ginsburg WM,
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                                                                                                         26-NOV-2002;
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99US-0123618P.
99US-0123957P.
99US-0125775P.
99US-0128849P.
                 02-MAR-2000; 2000WO-US005841
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                                                               99US-0131445P
                                                                           99US-0134287P
                                                                                       99US-0141037P
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                                                                                                        99US-0146222P
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99WO-US030
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Kabakoff RC, Lu Y, Pa
                                                                                                                                                                                                            080-086
                                                                                                                           99WO-US
                                                                                                                                                       SU-OW66
                                                                                                                                                                                          SD-OM66
                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                        WPI; 2000-572271/53.
P-PSDB; AAB33435.
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                                  10-MAR-1999;
12-MAR-1999;
23-MAR-1999;
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      14-SEP-2000
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04-MAY-1999
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8409.

1090.

Gurney AL, Hebert C, Henzel W; D, Shelton DL, Smith V; Wood WI, Yan M; Baker KP, Goddard A, iu Y, Pan J, Pennica umas D, Watanabe CK,

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

# Claim 23; Fig 43; 309pp; English

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-Dodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematoous, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogrem's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, peripheral netwous systems, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological

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                    graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
diseases of the lung, and transplantation associated diseases including
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                   Sequence 3759 BP; 774 A; 1205 C; 970 G; 810 T; 0 U; 0 Other;
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Title: Perfect score:

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Sequence 34465, Application US/10425115

Sublication No. US20040214272A1

GENERAL INFORMATION:
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APPLICANT:
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APP
Sequence 29, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 482, App
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                                                                                           US-09-978-295A-482
US-09-978-697-482
US-09-978-697-482
US-09-998-832A-482
US-09-978-189-482
US-09-978-189-482
US-09-978-181A-482
US-09-978-181A-482
US-09-978-181A-482
US-09-978-181A-482
US-09-99-833A-482
US-09-99-833A-482
US-09-998-834A-482
US-09-998-834A-482
US-09-998-834A-482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), OTHER INFORMATION: Clone ID: MRT4577_133259C.1
US-10-425-115-36465
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ORGANISM: Zea mays
       US-10-425-115-36465
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US-09-731-872-192
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Matches 59
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Sequence 192, App
Sequence 192, App
Sequence 184240,
Sequence 150417,
Sequence 52629, A
Sequence 7492, Ap
Sequence 7492, Ap
Sequence 122506,
Sequence 123506,
                                                                                                                                                                          6, 2005, 17:39:42; Search time 690 Seconds (without alignments) 9084.062 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
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US-09-731-872-192
US-09-876-997-192
US-10-425-115-184240
US-10-425-115-150417
US-10-425-115-5629
US-10-425-115-5629
US-10-352-7492
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US-10-424-599-122506
US-10-425-115-163680
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                               version :
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Gapop 60.0 , Gapext 60.0
                            GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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Match Length DB
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Publication No. US20040214272A1
Sublication No. US20040214272A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: 18-2132216
SEQ ID NOS: 369326
SEQ ID NO 15-4417
LENGTH: 222
                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 184240
LENGTH: 2121
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"Sequence 52629, Application US/10425115

"Sequence 52629, Application No. US20040214272A1

"Sequence 52629, Application No. US20040214272A1

"GENERAL INFORMATION: Thomas J.

"APPLICANT: Kovalic, David K.

"APPLICANT: Zhou, Yihua

"APPLICANT: Zhou, Yihua

"APPLICANT: Cao, Yongwei

"TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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5.1e-17;
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100.0%; Pred. No. 1.6e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_68706C.1
US-10-425-115-150417
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                                   Sequence 184240, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity 100.0°
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                           APPLICANT: Dumas Mine Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: JOBERT, Severin
TITLE OF INVERTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US 60/189,629
PRIOR APPLICATION NUMBER: US 60/189,629
PRIOR PLING DATE: 2000-12-08
PRIOR PLING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 192
LENGTH: 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 56; DB 9; Length 668; 100.0%; Pred. No. 1.6e-17; tive 0; Mismatches 0; Indels
Sequence 192, Application US/09731872
Patent No. US20020102604A1
GENERAL INFORMATION:
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; Sequence 192, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 56; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..203
US-09-731-872-192
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; LOCATION: 57..203
US-09-876-997-192
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Page 3

APPLICANT: Tao, Nengbing

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagam, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT PILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 7492

TYPE
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 122506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa. Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRANTSM: Bos taurus
COTHER INFORMATION: Clone ID: 32-LIB34-017-Q1-E1-H7
18-09-960-352-7492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 55; DB 9; Luilarity 100.0%; Pred. No. 5.1e-17; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.1e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_183771C.1
US-10-425-115-91860
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 538
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
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ORGANISM: Zea mays
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APPLICANT: SCRIEGE, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: 09/785,276
PRIOR PILING DATE: 2003-02-16
PRIOR FILING DATE: 2000-02-16
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/201,314
PRIOR FILING DATE: 2000-06-25
PRIOR PILING DATE: 2000-06-25
PRIOR PRIOR FILING DATE: 2000-06-25
PRIOR PILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-25
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-01-18
PRIOR PRIOR FILING DATE: 2000-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 369; 5.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_147996C.1
US-10-425-115-52629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.1%; Score 55; DB : 100.0%; Pred. No. 5.16 :ive 0; Mismatches
                                                                                                                                                                            FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 5.5629
LENGTH: 369
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
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Patent No. US20020137139A1
; GRNEAL INFORMATION:
; APPLICANT: Warren, Weeley C.
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Best Local Similarity 100.C
Matches 55; Conservative
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Best Local Similarity
Matches 55; Conserv
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ORGANISM: Zea mays
                                                                                                                                                        TITLE OF INVENTION:
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US-09-960-352-7492/c
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US-10-357-930-58429
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LENGTH: 376
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NAME/KEY: CDS
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US-09-803-589-13
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Sequence 163680, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: Acos, Thomas J.
APPLICANT: Application Solow, Yinha
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 163680
LENGTH: 838
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Sequence 29, Application US/09925301
Sequence 29, Application US/09925301
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 917
                                                                                                                                                          Query Match 5.1%; Score 55; DB 17; Length 787; Best Local Similarity 100.0%; Pred. No. 5.2e-17; Matches 55; Conservative 0; Mismatches 0; Indels
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                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_81629C.1
US-10-424-599-122506
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; OTHER INFORMATION: Clone ID: MRT4577_80852C.1
US-10-425-115-163680
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OTHER INFORMATION: unsure at all n locations
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                       TYPE: DNA ORGANISM: Glycine max
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US-09-925-301-29
LENGTH: 787
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GENERAL INFORMATION, Sean A.
APPLICANT: MCCATCHY, Sean A.
APPLICANT: HOLTZMAN, Douglas A.
APPLICANT: HOLTZMAN, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING PREVENTIVE, THERAPEUTIC AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: 07334-325001
CURRENT FILING DATE: 2001-03-09
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 60/054,666
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR PRILING DATE: 1999-09-01
PRIOR PRILING DATE: 1999-09-01
PRIOR PRILING DATE: 1999-09-01
PRIOR PRILING DATE: 1999-09-01
PRIOR FILING DATE: PASISEO FOR WINDOWS VERSION 4.0
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Publication No. US20040253605A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US/10/718,332
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: US/09/803,589
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                                                                                                                                                                                   958 ТАĞСААҺДАҚАҚАҚАҚАҚТАҚҚҚҚҚ 1012
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    Length 917;
                                                                                         Indels
Query Match 5.1%; Score 55; DB Best Local Similarity 100.0%; Pred. No. 5.2 Matches 55; Conservative 0; Mismatches
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Patent No. US20020112251A1
GENERAL INFORMATION:
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US-09-803-589-13
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Sequence 5349, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: AZIZ, Natasha
; APPLICANT: Glabburg, Wendy M.
APPLICANT: Glubburg, Wethods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TILE OF INVENTION: Methods 10.3.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT APPLICATION NUMBER: 60/429,739 ·
PRIOR APPLICATION NUMBER: 60/429,739 ·
PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5349
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/128,709
PRIOR FILING DATE: 1998-04
PRIOR FILING DATE: 1998-04
PRIOR PILING DATE: 1998-04
PRIOR APPLICATION NUMBER: US 60/054,645
PRIOR PILING DATE: 1999-08-04
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1999-08-06
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR PILING DATE: 1999-09-01
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SOUTWARE: PASESQ FOR WINDER: US 09/388,279
PRIOR PILING DATE: 1999-09-01
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: DCATION: (2063) ..(2063)

: THER INDEMATION: n is a, c, g, or t

US-10-723-860-5349
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; LOCATION: (106)...(630)
US-10-718-332-13
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ORGANISM: Mus musculus
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ORGANISM: Homo sapiens
FEATURE:
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US-10-723-860-5349
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IGGPGPDEKUNTRRVVDAFNUTALENVTAKEKKEINMGLSNYRYEKIKKLEEVRKELV
NKTRNKKALLGEIBGCPDDLQNIKLRNQTLESSAENVMGIRLPFVLVKTSRKARVEIE
ISDDSKPAHFEFNGAPFTLHDDLSILEGVRRNSIGRAGRATLH"
                                             AY224551 Oryza sat
AX449314 Sequence
AX44932 Sequence
BC013131 Homo sapi
BC01393 Homo sapi
CQ717592 Sequence
AX380911 Sequence
U18422 Homo sapien
BC082841 Xenopus 1
AX333694 Sequence
CQ48916 Sequence
CQ48916 Sequence
BC080383 Xenopus 1
AX449515 Sequence
AX469515 Genorhab
CQ581589 Sequence
AY008165 Caenorhab
CQ581589 Sequence
AY003183 Drosophila
AY065526 Drosophila
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.6%; Score 1084.2; DB 6; Length 1089; 99.7%; Pred. No. 9.4e-229; ive 0; Mismatches 3; Indels 0;
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Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C.
Mheat dp proteins and uses thereof
Patent: WO 0121644-A 1 29-MAR-2001;
CONSEJO SUPRATOR DE INVESTIGACIONES CIENTIFICAS
Location/Qualifiers
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Sequence 1 from Patent W00121644.
AX100704 GI:13619652
                                                             AP003335
AX449314
AX449520
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BC013993
CQ717592
AR380911
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AX333694
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BC080383
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AX449342
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AY224551
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97.8%; Score 1065.4; DB 8; Length 1083;
Best Local Similarity 99.0%; Pred. No. 1.3e-224;
Matches 1072; Conservative 0; Mismatches 11; Indels 0; Direct Submission Submitted (03-FEB-2000) Gutierrez C., C.S.I.C.-U.A.M. Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN Location/Qualifiers linear 9 mRNA for DP protein (dp gene).

Rice Full-Length cDNA Consortium, National Institute of

AUTHORS

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DEFINITION VERSION KEYWORDS SOURCE ACCESSION RESULT 3 AK111611

Oryza sativa (japonica cultivar-group) cDNA clone:J013105118, full insert sequence. FLI\_CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza. AK111611 AK111611.1 GI:37988274 ORGANISM

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fuylmura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashizaki, Y., Hayastsu, M., Hiramoto, K., Hiraoka, T., Hayashizaki, Y., Hayastsu, M., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Itda, Y., Ikeda, R., Imamura, K., Kadoh, H., Ida, J., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Komanata, M., Kodama, T., Kojima, K., Kojima, Y., Kohimoto, N., Kobayashi, M., Koya, S., Kuribara, C., Kurosaki, T., Kushimoto, N., Miyazaki, M., Matsubara, C., Kurosaki, T., Miura, J., Miyazaki, A., Mizubara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Madua, K., Murakani, K., Muraka, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Oka, M., Ooka, H., Osato, N., Otemo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Shinasaki, R., Shinahiki, T., Sogabe, Y., Sugami-Takeda, Y., Tagawa, A., Shiraki, Y., Sato, K., Satoh, K., Shiraki, K., Shinaki, K., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Shiraki, Y., Tagami, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yamamishi, A., Yasaki, J., Yamamishi, A., Yasaki, J., Yamamoto, M., Yasunishi, A., Yazaki, J., Yamanishi, A., Yananishi, A., Yana URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagada,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
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Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
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Genome Exploration Research Group in Riken Genomic Sciences Center
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Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
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Iida,Y., Sugano,S., Fuljimura,T., Suzuki,Y., Tsunoda,Y.,
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Submitted (12-58P-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 205-5602, Japan (E-mail:8Kluchi@mias.affrc.go.jp, Tel:81-29-818-7007, Fas.81-229-818-7007, Tax.81-229-818-7007, Pas.81-29-818-7007, Pas.81-20-818-7007, Pas.81-20-818-7007, Pas.81-20-818-7007, Pas.81-20-818-7007, Pas.81-20-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-818-7008-8 Yoshino, M. and Hayashizaki, Y.

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protein
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
  931 TGTCAAAACTCAAAACTGGCACCACCAGTTTCTTTGCACAGTTATGTATAGCTATAGCG 990
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                                                                   991 TACCTITCAGIAIGGAAACICGACCIAGITIAIAGAGACAGICICICAGGCIIIITTAGCAG
                                               ----TATCCTCATGAAAACTTGACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:39947"
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Direct Submission
Submitted (27-JAN-2003) Torrey Mesa Research Institute, S; Research and Technology, 3115 Merryfield Row, San Diego, (
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Pred. No. 4.6e-87;
0; Mismatches 133;
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/organism="Oryza sativa
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/isolate="21044"
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Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
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Yasunishi, A., and Hayashizaki, Y.
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/protein_id="CAC36471.1"
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Triticum monococcum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                        1 ATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTTAGGCGGAGAGTGTATGATGCT
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                                                                                                   317 ATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCT
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BT005286. GI:2895085?
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Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C.
Wheat dp proteins and uses thereof
Patent: WO 0121644-A 11 29-MAR-2001,
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
Location/Qualifiers
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                                    15.4%; Score 168; DB 6; I 100.0%; Pred. No. 1.3e-26; ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 168; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum monococcum"
/mol_type="unassigned DNA"
/db_xref="taxon:4568"
                                                                                                                                                                                                                                                                                                                                                     DNA
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Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
TITIGEGGAGCTGAAGTCCATTACGCAGAACGGTCTGGAGTTTGATGAGAAGAATATTAG 440
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                                                   AGTITGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAAT
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/mol_type="unassigned DNA"
/db_xref="taxon:4568"
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|protein_id="CAC36470.1"
|db_xref="G1:13619661"
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AX100712.1 GI:13619660
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Submitted (29-AUG-2001) Bergounioux C., UMR 8618, Cnrs, IBP bat
Universite Paris-Sud, 91405 Orsay, FRANCE
Location/Qualifiers
1..960
                                                                           13.1 AATGCGGTCCAAAGGAAGGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGAAGGCT
                                                                                                                            73 ACTCCAGTGAGAAGGAAATTGATTGTTGATGATTCTGAAATTGGATCAGAAGAAA
                                                                                                                                                                                                               ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGAAAAATAGTTTGTGAGAAA
                                                                                                                                                                                                                                                                                                                   193 TIGGAAGCCAAGAAGAAGATACTACAAGGAGGTIGCAGACGAAATTATTCAGATTTT
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Arabidopsis thaliana partial mRNA for E2F dimerisation partner
protein (dp2a gene).
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                          Indels
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dpza gene, ESF dimerisation partner protein.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
  Pred. No. 2.3e-23;
0; Mismatches 259;
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AFLKELREKVSLESIMSRNOBMVVKTQGPAGGFTLPFILLETNPHAVVEIEISEDMO
LVHLDFNSTPFSVHDDAYILKLMQEQKQEQNRVSSSSSTHHQSQHSSAHSSSSSCIAS
GTSGPVCWNSGSIDTR"
                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 879)
Chan, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Changes 1 to 879)

(Chan, M.W., Chenk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.W., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kaniya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Sondera, C.S., Pallm, C.J., Quach, H.L., Sakuran, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MSMEMELFVTPEKQRQHPSVSVEKTPVRRKLIVDDDSEIGSEKK
GQSRTSGGGLRQFSVMVCQKLEAKKITTYKEVADEIISDFATIKQNAEKPLNENEYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-MAR-2003) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collection and clustering of RAFL CDNAS (RAFL CDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAB: Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Chee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
                                                                              Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIS.
Location/Qualifiers
                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

    .879
    /note="putative DP-2 transcription factor"

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/note="This clone is in pUNI 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana"
                             Arabidopsis thaliana (thale cress)
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/protein_id="AAO63350.1"
/db_xref="GI:28950853"
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"mol_type="mRNA"
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KEYWORDS
SOURCE
ORGANISM
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Length 879

8

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Score 153.6;

14.18;

Query Match

612

709 672

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PAT 03-JUL-2002
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                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                            Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
Nucleic acid molecules encoding plant cell cycle proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                             linear
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14.1%; Score 153.6; DB 6;
Best Local Similarity 55.6%; Pred. No. 2.4e-23;
Matches 350; Conservative 0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana"
                                                                                                             DNA
    751 AATAGCACACCTTTCTCGGTCCATGATGAT 780
                                                                                                                                                                                                                                                                                                                                                                                                               Patent: WO 0185946-A 16 15-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis tha
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                                                                           1114 bp
from Patent W00185946.
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Location/Qualifiers
                                                                                                                                                                       AX449297.1 GI:21698044
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AX449297
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DEFINITION
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KNIRRRVYDALNVFWALDIIARDKKEIRWKGLPITCKKOVEEVKÜNRRRVMSSVQKKA
KRIRRRVYDALNVFWALDIIARDKKEIRWKGLPITCKKOVEEVKÜNRRRVMSSVQKKA
AFKELLERVKVSSLESIMSRNQBWVKTQCPARGFTLPFILLETNPHAVVEIEISEDWQ
AVHLDFNSTPFSVHDDAYILKLMQEQKQEQNRVSSSSSTHQSQHSSAHSSSSSCIAS
GTSGPVCWNSGSIDTR"
                                                                                                                                                                                                                                                                                                                                                                                                          translation="mSMEMELFVTPEKQRQHPSVSVEKTPVRRKLIVDDDSEIGSEKK/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                /codon_start=1
/product="E2F dimerisation partner protein (DP2a)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 153.6; DB 8; Length Pred. No. 2.4e-23; 0; Mismatches 259; Indels
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/db_xref="UniProt/TrEMBL:Q9FNY3"
  thaliana'
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                                                                                                                                                                                                                                                       /function="transcription"
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/db_xref="G1:18447786"
                    /mol type="mRNA"

/cultivar="colombia"

/db xref="taxon:3702"

/tissue type="buds"

/dev stage="flowering"

1. .960
organism="Arabidopsis
                                                                                                                                                                                /gene="dp2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%;
                                                                                                                                                 /gene="dp2a"
                                                                                                                                                                                                                                        gene="dp2a"/
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Matches 350; Conserv
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FEATURES

DEFINITION

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131 AATGCGGTCCAAAGGAAGGGGCCTGTTGACCCGGATAAAGATAGGAAGAAGAAGGAGGAGAAGGT 190
                                                               196 GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG 255
                                                                                                                                                                                                                                                                                                                                                              ATAAGGCGGAGAGTCTACGATGCGCTCAATGTGTTTCATGGCGTTGGATATTATTGCAAGG 435
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                             256 TTGGAAGCCAAGAAGATAACTACTACAAGGAGGTTGCAGACGAAATTATTTCAGATTTT 315
                                                                                                                                                                                                                                                                            316 GCCACAATTAAGCAAAACGCAGAAGCCTTTGAATGAAATGAGTACAATGAGAAGAAC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 GATAAAAAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAA 495
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                          GCGCCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                           GITGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
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Nucleic acid molecules encoding plant cell cycle proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1189;
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Location/Qualifiers
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GOSRTSGGGERQFSVAVCQKLEAKKITTYKEVADETISDFATIKQNAEKPLNENEYNE
KNITRRVYDALNVFMALDITABDKKETTRWKGLPTTCKKOVEEVKMDSNVCMSSVQKKA
AFLKELREKVSSLESELMSRNOEMVKTYQFPAEGFTLPFILLETNPHAVVEIELSEDMO
LVHLDFNSTPFSVHDDAYILKLMQEQKQBQNRVSSSSSTHQSQHSSABASSSSCIAS
                                                                                                                                                                        Arabidopsis thaliana At5902470 mRNA for putative DP-2 transcription factor, complete cds, clone: RAFL16-67-D16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           et
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                                                                                                                                                                                                                                                                                                                                                         Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An Arabidopsis full-length cDNA library was constructed essential as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145; cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLG-1-B vector (Carninci al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is in a modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Arabidopsis thallana full-length CDNA
Published Only in Database (2002)
2 (bases I to 1121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@gsc.riken.go.jp, Tel:81-45-503-9625, Fax:81-45-503-9586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                      mRNA
1. 1121
/gene="At5g02470/T22P11_60"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                      1121 bp
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/db_xref="taxon:3702"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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A method to modify cell number, architecture and yield of plants loverexpressing the e2f transcription factor
Patent: WO 03025185-A 3 27-MAR-2003;
CropDesign N.V. (BE)
                                                                                                              GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG
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/mol_type="unassigned DNA"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/mol_type="unassigned DNA"
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Direct Submission
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Submitted (06-SEP-2000) Magyar Z., Department Plantgenetica,
Submitted (06-SEP-2000)
Bornatorium voor Genetica, Universiteit Gent, K.L. Ledeganckstraat
35., B-9000, Gent, BELGIUM
Location/Qualifiers
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                                                                                     GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG 365
                                                                                                                 GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG 310
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AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGGAGAAGGCT 190
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                                                                                                                                              36 TTGGAAGCCAAGAAGATAACTACTTACAAGGAGGTTGCAGACGAAATTATTTCAGATTTT 425
                                                                                                                                                                         AAGTCCAT--------GGCACATATTGGTCAAGGTTTGATGAAGAAT 352
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                                                          GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACACAAAATAGTTTGTGAGAAA
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Arabidopsis thaliana mRNA for DP-like protein (dpa gene) .
AJ294531
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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GTSGPVCMNSGSIDTR"
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                                                                                                                                                                                                                 gene="dpa"
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      thaliana"
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PAT 10-APR-2001
                                                                                                   Triticum monococcum
Triticum monococcum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                       Gutierrez-Armenta, C.C. and Ramirez-Parra, E.C. Wheat dp proteins and uses thereof Patent: WO 0121644-A 7 29-MAR-2001; CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES) Location/Qualifiers
                                linear
                                                                                                                                                                                                                                                              1. 153
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Sequence 7 from Patent W00121644.
AX100710 GI:13619658
RESULT 15
AX100710
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164 GATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGC 223 0; Gaps 14.0%; Score 153; DB 6; Length 153; 100.0%; Pred. No. 2.6e-23; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 153; Conservative ઠે

1 GATAAAGATAGGAGAAGAAGAGGTGCGGCACCGAGGATCACCGGTTGGGGCTCCGC 60

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Search completed: February 6, 2005, 14:35:10 Job time : 5151 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

February 6, 2005, 12:23:21; Search time 697 Seconds (without alignments) 9249.065 Million cell updates/sec Run on:

US-10-088-830-1 1089 Title: Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 seqs, 2959870667 residues Searched:

Potal number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04: Database :

genesegn2003ds:\* genesegn2004as:\* genesegn2004bs:\* geneseqn2003cs: geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2002bs: geneseqn2002as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Add36842 Cell prol Adk71795 Rice endo Adk71795 Rice endo Ad68159 Transcrip Ad62852 Transcrip Ad62852 Transcrip Ad62844 Transcrip Ad62847 Arabidops Aa896319 Arabidops Ad85559 Dimerisat Ac45100 Arabidops Ad65559 Dimerisat Ad65559 Dimerisat Ad65559 Arabidops Aaf80144 Nucleotid Description SUMMARIES ADQ36842 ADK71795 ADC83159 AAF80148 ADC62852 ADC62852 ADC62859 ADC62859 AAKS96319 ACC45100 ADC63626 ADC636 ADC63626 ADC636 ADC63626 ADC63626 ADC63626 ADC63626 ADC63626 ADC63626 ADC63626 ADC63626 ADC63626 ADC636 AAF80144 Query Match Length DB 168 1587.6 155.2 1155.2 1153.6 1153.6 1153.4 1153.4 1153.4 1150.8 1150.8 Score So. Result

AAA59702 DNA encod	2 ADO63363 Ado63363 Transcrip	AAZ34580 Corn DP-2	2 ADQ36854 Cell pro	2 ADQ36844 Cell prol	2 ADO63216 Ado63216 Transcri	2 ADO62851 Transcrip	AAS96304 Arabidops	2 ADO63362 Transcrit	AAS96415 Arabidops	3 ADR65325 Cotton cD	ACN88986	l ADI32130 Human cDN	2 ADN05729 Antipsori	4	AAS92244 DNA encod	3 ACN38014 Acn38014 Tumour-as	4	8	7 Aaz34577	Aas96410	AAS96332 Arabidops	AAV72862 Caenorhat	ABL08071 Abl08071 Drosophi	LOTULO RE
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138.2	138.2	136.6	136.2	132.2	127.8	123	118.6	115	104.6	102.8	99.2	98.8	98.8	97	97	97	97	97	95.2	93.6	93.6	88	88	9

## ALIGNMENTS

RESULT 1 AAF80144

ВЪ. AAF80144 standard; DNA; 1089

AAF80144;

11-JUN-2001 (first entry

Nucleotide sequence of a wheat E2F-dimerisation partner (DP) protein.

E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation; 

Triticum monococcum.

Location/Qualifiers 20. .805

/\*tag= / a /product= "E2F-dimerisation partner (DP) protein"

WO200121644-A2

29-MAR-2001

25-SEP-2000; 2000WO-EP009325

99ES-00002127 99ES-00002474 24-SEP-1999; 11-NOV-1999; (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

Gutierrez-Armenta C, Ramirez-Parra

WPI; 2001-257972/26. P-PSDB; AAB67762.

New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.

Claim 13; Fig 1; 77pp; English.

Adresold DNA fragm Adresold DNA fragm Adocase Transcrip Adocase Transcrip Adocase Arabidops Adosolo DNA fragm Adresolo DNA fragm

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protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F-DP domain. DP proteins can be medulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size
encodes a E2F-dimerisation partner (DP) protein. The
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Sequence 1089 BP; 367 A; 215 C; 261 G; 246 T; 0 U; 0 Other;

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                                                         GGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGT
                                                                                                                                                                                                                                                                                    TTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTA
                              Gaps
  Length 1089;
                              0
                              3; Indels
  DB 4;
  Score 1084.2; DB 4,
Pred. No. 5.2e-207;
0; Mismatches 3;
99.6%;
                 Best Local Similarity 99.7
Matches 1086; Conservative
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encoding a cell proliferation related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.
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                            CTTGACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGATTTTAACCTGCAAATTTTG
                                                                                                                                                                                                                                                     AGAACTGGCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATATATCCTCATGAAAA
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ress response; ds.
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40.6%; Score 442.2; DB 12; 79.8%; Pred. No. 8.7e-79; tive 0; Mismatches 133; ...

Query Match 40.6 Best Local Similarity 79.8 Matches 548; Conservative

Length 885;

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The present invention describes rice endosperm specific expression sequence labels (expressed sequence tag (EST)) comprising the 48 cDNA sequences, given in SEQ ID NO:1 to 48. The expression sequence labels can be combined in a gene chip using the microarray technique. The expression sequence labels are useful for DNA sequence determination of constitutive rice endosperm cDNA library, removing redundant sequences, and searching interconnection network data bases. The chip can be used for gene cloning, early prediction of hybrid vigour, safety detection of transgenic agricultural product, screening new-type herbicides and pesticides.
                                                                                     expression sequence labels useful for
                                                                                                                                                                                                                                                                                                               Sequence 548 BP; 164 A; 118 C; 112 G; 154 T; 0 U; 0 Other;
                                                                                                                            Claim 1; SEQ ID NO 31; 28pp; Chinese.
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nilarity 71.1%;
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                        TTATTCAGAGCTGAAGTCCATGCCACATATTGGTCAAGGGTTTTGATGAGAAGAATATTAG
                                                                                                                                                                                           TTTTGCGGAGCTGAAGTCCATTACGCAGAACGTCTGGAGTTTGATGAGAAGAATATTAG
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                                                                                                            AGTITIGIGAGAAAGTITGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAAT
                                                                                                                                                                                                                                                    GCGGAGGGTATATGATGCTTTCAATGTGCTTTGCAATTCGTGTTATTGCAAAGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice endosperm expressed sequence tag (EST) SEQ ID NO:31
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|GCACCACCAGTTTCTTTTGCACAGTTATGTATAGCTATAGCGTACCTTTCAGTATGGAAA
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                                                                                                                    GACCTTCCAGAATATACATTACGCAACCAGGCTAGTCAGAGGCCCA-CAGAAAGTGTTAAT
                                                                                                                                                             GGCATCCGCCTTCC-ATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAATTGA
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                                         Gaps
                                         19;
  Length 548;
                                         Indels
Score 218; DB 10;
Pred. No. 4.8e-34;
0; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD063159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO63159
ID ADO6
XX
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RESULT

31-OCT-2001; 2001CN-00132498

ADO63159

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Increased collected from increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to heat, increased colerance to heat, increased colerance to permination in heat, increased tolerance to heat, increased tolerance to germination in heat, increased tolerance to germination in heat, increased tolerance to conditions, increased tolerance to increased tolerance to multiple fungal pathogens, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABC, altered sugar sensing, increased tolerance to sugars sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, altered carbon/nitrogen sensing, altered track about meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced captering, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced aptered trichome structure altered coldevelopment, altered shade aptered trichome structure altered coldevelopment, altered sendered shade captered trichome structure altered coldevelopment, altered sendered captered trichome structure altered coldevelopment, altered sendered capteriation, altered sendered captered trichome structure, altered captered trichome attered trichome development, altered sendered trichome altered captered captered captered sendered captered captered captered captered sendered captered sendered captered c
                                                                                                                                            Plant; transcription factor; transgenic plant; abiotic stress tolerance; sembicis stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                              Transcription factor G2981 orthologous sequence, SEQ ID 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant polynucleotide encoding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1626; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heard JE, Ratcliffe O, C
JL, Haake V, Dubell AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2002; 2002US-0411837P.
17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-2003; 2003WO-US030292.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-330163/30.
                                                                                                                                                                                                                                                                                                                     WO2004031349-A2.
                                           15-JUL-2004
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475
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                                                                                                                                                                   672
                                                                                                                                                                                                                              732
                                                                                                                                                                                                                                                     120 GATTICGGAAGATTCAAAGTTTGCACGGTTCGACTTCAACGGTGCACCATTCACCATGCA 179
                                                                                                                                                                                                                                                                                         792
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                                                                                                                                                                                                 60 GGCATCCTTCCGGTTCTTATTGATCAAGACATCCCGAAAAGCAAGGGTGGAAATTGA 119
                                                                                                                                                                                                                                                                                                                                                                                                                  848 GCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATA-----TATCCTCATGAAAA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 TTATGTATAAACTCATTGCCGTTTCAATTCGAAGCTTGTGTACAAGCTCCATTGATGAAA 535
                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                180 IGAIGHAICHAICCTIGAAGCCATCAGGCGIAACAACAAAGGAAGAGCTGGCCTCC
                                                                                                                                                                                                                                                                                                                                                     793 CACCCTTCACT-AGAGACTCAAGAATATTACAAATGAATTAAAAGTG----TTAGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 GCCTCTTTTTGTGCCTAGCAGGTGA----GTCTGGAATAGTTTTTTTTTGCGTGTGCTG
                                                                                                        554 GATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTAAT
                                                                                                                                    1 GACCTTCCAGAATATACATTACGCAACCAGGCTAGTCAGAGGCCA-CAGAAAGTGTTAAT
                                                                                                                                                                   614 GGCATCCGCCTTCC-ATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAATTGA
                                                                                                                                                                                                                                GATTTCAGATGACTCGAAGTTTGCCCCATTTCGAGTTCAATGGTGCACCATTCACATTGCA
                                                                                                                                                                                                                                                                                           TGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGCTGGCCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGACCTAGTTTATAGGACAGTCTCTCAGGCTTGAGAAGA-TTTTAACCTGCAAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCGACCTAGTTTATAGGACAGTCTCTCAGGCTTTTTAGCAGATATGACCTGCGAATTTT
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein.
                                                                         19;
                                           DB 12; Length 548;
            C; 112 G; 154 T; 0 U; 0 Other;
                                                                         Indels
                                         / Match 20.0%; Score 218; DB 12; Local Similarity 71.1%; Pred. No. 4.8e-34; Les 391; Conservative 0; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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            Sequence 548 BP; 164 A; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF80149 standard; DNA; 168
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11-NOV-1999;
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Matches
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Reuber TL;

Adam LJ, Re Sherman BK;

Creelman RA, Keddie JS,

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AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAACGITCTCATTGCACTTCGTGTTATTGCAAAAGAAAAAAAGGAGATACGGTGGATG 120
                                                                           New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCACATATTGGTCAAGGGTTTGATGAGAAAAAATATTAGGCGGAGAGTGTATGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 ATGGCACATATTGGTCAAGGGTTTGATGAGAATATTAGGCGGAGAGTGTATGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%; Score 168; DB 4; Length 168; 100.0%; Pred. No. 3.7e-24; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 GGCCTTTCAAATTACAGATATGAAAAAAAAAAAAGAAGCTTGAGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 168 BP; 59 A; 19 C; 44 G; 46 T; 0 U; 0 Other;
                                                                                                                                                       Disclosure; Page 73-74; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEND-) MENDEL BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 168; Conservative
                         WPI; 2001-257972/26.
P-PSDB; AAB67766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                    AAF80146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblactoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblactoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
                                                                                                                              New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605 AATGITAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 168 BP; 62 A; 38 C; 33 G; 35 T; 0 U; 0 Other;
(CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.7e-24;
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                                      Ramirez-Parra E;
                                                                                                                                                                                                       Disclosure; Page 74-75; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gutierrez-Armenta C, Ramirez-Parra
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99ES-00002474
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                                      Gutierrez-Armenta C,
                                                                         WPI; 2001-257972/26.
P-PSDB; AAB67767.
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11-NOV-1999;
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AAF80148
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Gaps

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Plant; transcription factor; transgenic plant; abiotic stress tolerance; sometic stress tolerance; low nitrogen tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                   Reuber TL;
                                                                                                                                                 Franscription factor G2981/2982 orthologous sequence, SEQ ID 1319
484
                     168
                                                                                                                                                                                                                                                                                                                                                                                                   Adam LJ, Re
Sherman BK;
            GGCCTTTCAAATTACAGATAAGAAAAAATAAAGAAGCTTGAGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                  Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
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CCTTTCAAATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGT 498

439

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Werri, 2004-330163/30.

We recombinant polyvuoleotide encoding transcription factor
properties useful for producing transgenic plants with advantageous
properties compared to a reference plant.

Compared to 1319; 510pp; English.

The present invention relates to novel plant transcription factor
compared to the used to produce transgenic plants, which oversapess
(III) where the transgenic plant or which type plant increased tolerance to cold,
increased tolerance to sometic stress, increased tolerance to cold,
increased tolerance to sometic stress, increased tolerance to cold,
increased tolerance to sometic stress, increased tolerance to cold,
increased tolerance to sometic stress, increased tolerance to cold,
increased tolerance to low nitrogen conditions, increased tolerance to cold,
increased tolerance to low nitrogen conditions, increased tolerance to
grammation in heat, increased tolerance to disease including
increased tolerance to low nitrogen conditions, increased tolerance to
grammation in heat, increased tolerance to disease including
increased tolerance to low nitrogen conditions, increased tolerance to
grammation with the timerages enablishing pathogens, increased tolerance to
low phosphate conditions, increased tolerance to
low phosphate conditions, increased tolerance to
low phosphate submonfulity to ABA, reduced sensity, increased tolerance to
low phosphate conditions, altered tolerance to discarce
to sugars, altered flower terred track development, altered send track development, altered send development, altered tolerance tolerance, altered tolerance, altered
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                                                                             TGTTGACCCGGATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGATCACCGGTTG 213
                                                                                                                                                                                              AGGICTCCCCCAATITAGIATGAAAGIGIGIGAGAAGGIAGAAAAAGCAGGGGAAGAACACAC 376
                                                                                                                                                                                                                                                                            ATACAATGAGGTGGCGGATGAGCTTGTTGCTGAATTTTCTGAACCAAGCAATAGTGAATT 436
                                                                                                                                                                                                                                                                                                                 GGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCTTT 378
                                                                                                                                                                                                                                                                                                                                                                                            GCCCCCTGATCAGCAACAATATGATGAAAAAAAACATCCGCCGAAGGGTCTATGATGCTCT 496
                                                                                                                  GGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAAC
                                                                                                                                                                                                                                       -GAAGTCCAT
                                        Gaps
                                      18;
14.5%; Score 157.6; DB 12; Length 56.1%; Pred. No. 6.8e-22; ive 0; Mismatches 254; Indels
                    Local Similarity 56.1
nes 348; Conservative
                                                                                                                                                                                                                                                                          377
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   Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (MD061534-AD06379B). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to cold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                             TTCAGATGACTCGAAGTTTGCCCCATTTCGAGTTCAATGGTGCACCATTCACATTGCATGA
                                      CAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTTTGATGATCT
                                                                                                      CCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAAATGTTAAT---GG
                                                                                                                                                                         616 CATCCGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCCAAGGGTGGAAATTGAGAT
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Sherman BK;
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Haake V, Dubell AN,
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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P-PSDB; ADO63085.
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cc increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, increased tolerance to low phosphate conditions, increased tolerance to conditions, increased tolerance to conditions, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ACC, altered sugar sensing, increased resistance to sugars, altered carbon/nitrogen sensing, early flowering, late to sugars altered flower structure, loss of flower determinacy, reduced fertility, altered flower structure, loss of flower determinacy, reduced apical dominance, altered vascular tissue structure, reduced altered stem morphology, altered vascular tissue structure, reduced altered seed development, altered development, altered seed conditions, altered seed conditions, altered seed avelopment, altered seed conditions, altered seed coloration, altered cell expansion, altered phase change, altered seed coloration, altered cell expansion, altered plants, increased cell expansion, altered plants, death content, altered seed coloration, altered seed coloration altered seed colorations altered seed colorations al 418 532 GAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAA---ACACTG 589 251 GTTGAAGCCAAAGGAAGAACAACAATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG 310 311 AAGTCCAT-------GCACATATTGGTCAAGGTTTGATGAAGAAT 352 419 GCCACAATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAAC 478 ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412 ATAAGGCGGAGAGTCTACGATGCGCTCAATGTGTTCATGGCGTTGGATATTATTGCAAGG 538 539 GATAAAAAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAGGATGTGGAAGAA 598 GTCAÁGATGGATCGTAATAAAGTTATGAGCAGTGTGCAAAAGAAGGAGCTGCTTTTCTTAAA 658 239 ACTCCAGTGAGAAGGAATTGATTGTTGATGATTCTGAAATTGGGTCAGAGAAA GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG 359 Tragaagccaagaagaracracracaagaggrigcagacgaarrarricagarrir CTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAG Gaps 21; Length 1267; Sequence 1267 BP; 420 A; 225 C; 267 G; 355 T; 0 U; 0 Other; Pred. No. 2e-21; 0; Mismatches 258; Indels Score 155.2; DB 12; ftp.wipo.int/pub/published\_pct\_sequences. 14.38; 55.78; Best Local Similarity 55.7 Matches 351; Conservative 299 353 479 191 599 533 Query Match 413 473 a à ઠે a ò g ò 유 ò 유 Š 셤 ò 셤 ò

GAGTTGAGAGAAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAAATCAAGAGATGGTT 718 590 GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCT 649 Greangacreangeceraceagangaritracerracearrearrearrengagacane 778

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fungal disease and particularly Erysiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/futrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced altered stem morphology, altered development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced appical dominance, altered trichome density, altered trichome development, altered trichome structure, altered shade 709 779 CCTCACGCAGTAGTCGAAATCGAGATTTCTGAAGATATGCAACTTGTACACCTCGACTTC 838 Plant; transcription factor; transgenic plant; abiotic stress tolerance; sometic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds. avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation, The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (AD061534-AD063778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant. 650 AGGAAAGCAAGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTC Reuber TL; Adam LJ, Re Sherman BK; Transcription factor G2981 coding sequence, SEQ ID 611. Creelman RA, Keddie JS, 710 AATGGTGCACCATTCACATTGCATGATGAT Claim 1; SEQ ID NO 611; 510pp; English. Ratcliffe O, C V, Dubell AN, (MEND-) MENDEL BIOTECHNOLOGY INC. ADO62144 standard; DNA; 1267 18-SEP-2002; 2002US-0411837P. 17-DEC-2002; 2002US-0434166P. 24-APR-2003; 2003US-0465809P. 18-SEP-2003; 2003WO-US030292 15-JUL-2004 (first entry) Heard JE, R Arabidopsis thaliana. WPI; 2004-330163/30. P-PSDB; ADO62145. WO2004031349-A2. Riechmann JL, 15-APR-2004 ADO62144; ບ້ Jiang 원 à 셤

Arabidopsis cDNA encoding partial cell cycle protein CCP16.

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altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light altered seed coloration, altered seed size, altered seed size, altered seed size, content, altered seed coloration, altered seed size, altered seed size, altered seed oil content, altered seed protein content, altered seed protein content, altered seed oil altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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The invention relates to a novel cell cycle protein (CCP) and the colymucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and anni-CCP antibody is useful for modulating the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle progression is useful for modulating the cell cycle progression in plants. CCP is useful to treat regulating cell cycle progression in plants. CCP is useful to treat and canola. CCP modulating of protein or production of CCP protein forms which have decreased or absorber compounds that bind to or modulating agents in captured care useful as herbicides or plant growth regulators. The polypeptide are useful for modifying cell fate, plant development, collypeptide are useful for modifying cell fate, plant development, collypeptide are useful as herbicides or plant growth regulators. The polyputchectide is useful for modifying cell fate, plant development, collypeptide are useful as herbicides or plant growth regulation, promotion, stimulation or mhancement of cell division, bnA replication, premotion, stimulation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, continitiation and/or development, module furction, dwarfism in plants, continitiation and/or development, module furction, dwarfism in plants, containing the plants of the cell cycle of a plant string activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, averlopment, endoreduplication in storage cells, storage tienes and/or development, enhance crop yields and attendate e.g. enhance crop yields and attendate of a protein involved in the cell cycle due to convirue cycle organs of plants or its parts. CCP is useful as useful as an immunogen to convint con contraing CCP substrates. The po 131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGGAGAAGCT 190 86 ACTCCAGTCAGAAGGAAATTGATTGTTGATGATTGATTTGGATTGGATCAGAGAAA 145 Cell cycle protein; CCP; ss; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; occurring CCP substrates. The polynucleotide is useful for expressing CCI protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators. 21; Gaps Length 1114; Sequence 1114 BP; 378 A; 197 C; 243 G; 296 T; 0 U; 0 Other; .; Z Indels De Veylder L, Acosta JAT, Magyar Score 153.6; DB 6; Pred. No. 4e-21; 0; Mismatches 259; nutrient deprivation; pathogen attack; crop yield Claim 38; Fig 16; 316pp; English. 14-MAY-2001; 2001WO-IB001307. (2-MAY-2000; 2000US-0204045P. tch al Similarity 55.6%; 350; Conservative (CROP-) CROPDESIGN NV. Arabidopsis thaliana. WPI; 2002-062249/08. P-PSDB; AAU72497. Boudolf V, Local Similarity WO200185946-A2 15-NOV-2001 nvention Query Match 'n Inze 셤 8

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AAS96287 standard; cDNA; 1114 BP

RESULT 1( AAS96287

(first entry)

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GCGCCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis cDNA encoding cell cycle protein CCP16.
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                                                                                                             311 AAGTCCAT-----
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P-PSDB; AAU72529.
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The invention relates to a novel cell cycle protein (CCP) and the polymucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample A CCP modulator is useful for modulating the cell cycle protein to read and polypeptide molecules are useful as modulating agents in neits, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP mucles of acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or protein or production of CCP protein forms which have decreased or protein or production of CCP protein forms which have decreased or protein or production of CCP protein forms which have decreased or polymorleotide is useful for modifying cell fate, plant development, of polymorleotide is useful for modifying cell fate, plant development, to polymorleotide is useful for modifying cell fate, plant development, to stimulation or enhancement of cell division, blant plants, stimulation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, module function, development, endicated acceptance or resistance to stress. CCP, the polymorleotide and the anti-CCP antibody are useful in agriculture to modulate the continuous and attendate or activity, of a protein involved in the cell side to protein land, heat, drought, salt stress, or biotic stress such as cold, mutrient deprivation, heat, drought, salt stress, or biotic stress such as environmental conditions, including abiotic stress such as infunded acceptage cells, storage tells, corage organs of plant architecture, plant quality traits, plant reproduction and see
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New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 ACTCCAGTGAGAAGGAAATTGATTGTTGATGATGATTTCTGAAATTGGATCAGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 GGGCAATCAAGAACTTCTGGAGGCGGGCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG
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Pred. No. 4.1e-21;
0; Mismatches 259;
                                                                                                            Claim 38; Fig 16; 316pp; English.
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Best Local Similarity 55.6%;
Matches 350; Conservative
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461 GATAAAAAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGA 473 CTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAG

353 ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412

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DB 10;

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726 ĠTGÀAGAĊTCAĠGCCCAĠCAGÀAĠĠATŤTACĊTŤAĊĊĂŤŤĊAŤTCŤACŤTGÄĠÄĊÄAAC 785
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                                                                                                                                           246 ACTCCAGTGAGAAGGAAATTGATTGTTGATGATTCGAAATTGGATCAGAGAAGAA 305
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                                                                                                                                                                                                                                                                                               251 GTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
                                                                                               AATGCGGTCCAAAGGAAAGGAGCTGTTGACCCGGATAAAGATAGGAAGAAGAAGAAGCT
                                                                                                                                                                                                                                                                                                                                              366 TİGGAAĞCCAAGAAGATAACTACATACAAGGAĞĞTIĞCAĞAĞĞAĞATTATİTÇAĞATTİT
                                                                                                                                                                                                                                                                                                                                                                                                  --GGCACATATTGGTCAAGGGTTTGATGAGAAT
                                                                                                                                                                                                  GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
Score 153.6; DB 10;
Pred. No. 4.2e-21;
0; Mismatches 259;
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/product= "DP protein"
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174. .1052
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  atch 14.1%;
cal Similarity 55.6%;
350; Conservative
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       Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to increasing the cell number of specific cell types, specific tissues or specific organs in a plant comprises modulating the expression and/or the activity in the specific cell types, specific tissues or specific organs of the plant E2F transcription factor. The E2F transcription factor or its homologue, derivative or fargment, is useful for prolonging the period of cell division in certain cells and tissues, for increasing the period of cell division in certain cells and tissues, for increasing the period of cell division in certain cells and tissues, for obtaining seedlings with enhancing expedings, for obtaining plants thaving more cells in a particular tissue, for obtaining plants having more cells in a particular tissue, for obtaining plants having more cells in a particular tissue, for obtaining plants having more cells in a particular tissue, for obtaining plants having the cells to re-enter the cell cycle, for overriding the cell differentiation signals, or for altering cell shape.

The present sequence represents the dimerisation partner encoding
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members of the plant E2F
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                                                                                                                                                                                                                                           GAGTTGAGAGAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAATCAAGAGAGGTGGTT 640
                                                                                                               649
                                                                                                                                                           641 ĠTGAAGAĊTCAAĠGCCCAĠCAGAAĠĠATŤTACĊTŤAĊĊĀŤTĊAŤTCŤACŤTGĀĠĀĊĀAAC 700
                                                                                                                                                                                                               650 AGGAAAGCAAGGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTC
               GAAATCGAAAAACAGTTTGATGATCTCCCAAAACATCAAGTTACGTAACCAA---ACACTG
                                                                                                               GAAAGCTCAGCAGAGAATGTTAATGGCATCCGCCTTCCATTCGTATTGGTCAAGACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broekaert W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene therapy; stress resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying cell number, architecture and yield of modulating the expression and/or the activity of transcription factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D, Mironov V,
                                                                                                                                                                                                                                                                                                                 AATGGTGCACCATTCACATTGCATGAT 739
                                                                                                                                                                                                                                                                                                                                                Dimerisation partner encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3; 41pp; English
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Dillen W, Frankard V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CROPDESIGN NV
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Dillen W,

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Arabidopsis thaliana, modulation, endoreduplication, plant, transgenic plant, cell cycle, E2F; DP; gene, ss.
                                        Arabidopsis thaliana DP encoding cDNA SEQ ID NO:3
                                                                                                                             WO2003018818-A2
                                                                                                                                          06-MAR-2003
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Sequence 1274 BP; 420 A; 228 C; 271 G; 355 T; 0 U; 0 Other;

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expression or activity of an E2F and DP gene or polypeptide. Also described: (1) a transgenic plant cell overexpressing an E2F and described: (1) a transgenic plant cell overexpressing an E2F and gene, or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP gene or an E2F and DP are plant, or a part of the plant, comprising the cells described above; (3) a progeny of the plant described above. The method is useful in modulating plant cell cycle proteins by modifying the expression or activity of an E2F and DP gene or polypeptide. The present sequence encodes Arabidopsis thaliana DP, which
                                                                                                                                                                                                    Modulating endoreduplication in a plant, or a part of the plant, comprises modifying the expression or activity of an E2Fa and DPa gene or
                                                                                                                                                                                                                                                                                                       The present invention describes a method for modulating endoreduplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1274 BP; 420 A; 228 C; 271 G; 355 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used in the exemplification of the present invention
                                                                                                                   Mironov V, Segers G;
                                                                                                                                                                                                                                                                         Disclosure; Page 25-26; 34pp; English.
                 26-AUG-2002; 2002WO-EP009504.
                                                 24-AUG-2001; 2001US-00938342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.6%;
Matches 350; Conservative
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                                                                                                                   De Veylder L, Inze D,
                                                                                 (CROP-) CROPDESIGN NV.
                                                                                                                                                    WPI; 2003-300735/29.
                                                                                                                                                                    P-PSDB; ABP96848
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The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (11) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises can altered trait selected from increased tolerance to ablotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to heat, increased commination in heat, increased tolerance to heat, increased tolerance to low phosphate conditions, increased tolerance to low phosphate conditions, increased tolerance to low phosphate conditions, increased tolerance to low phosphate conditions, increased tolerance to multiple fungal pathogens, increased resistance to phybosate, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered flower structure, loss of flower determinacy, reduced fortility, altered carbon/nitrogen sensing, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced epical dominance, altered trichome density, altered trichome development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; transcription factor; transgenic plant; abiotic stress tolerance; semotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             altered trichome structure, altered root development, altered shade avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation,
                                     786 CCTCACGCAGTAGTCGAAATCGAGATTTCTGAAGATATGCAACTTGTACACCTCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
650 AGGAAAGCAAGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reuber
                                                                                                                                                                                                                                                                                                                                                                                                        Transcription factor G2981/2982 orthologous sequence, SEQ ID 2093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cliffe O, Creelman RA,
Dubell AN, Keddie JS,
                                                                                                                                846 AATAGCACACCTTTCTCGGTCCATGATGAT 875
                                                                                            710 AATGGTGCACCATTCACATTGCATGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2093; 510pp; English.
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Riechmann JL, Haake V, Dubell A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                ADO63626 standard; DNA; 1153
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24-APR-2003; 2003US-0465809P.
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                             AD063626;
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ID ADO6
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                                                                                                                                원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATCGAAAAACAGTTTGATGATCTCCAAAACATCAAGTTACGTAACCAA---ACACTG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 ACTCCAGTGAGGAAATTGATTGTTGATGATGATCTGAAATTGGATCAGAGAAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 GGGCAATCAAGAACTTCTGGAGGCGGCCTTCGTCAATTCAGTGTTATGGTTTGTCAGAAG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GGCACATATTGGTCAAGGGTTTGATGAGAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 GCCACAATTAAGCAAAACGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAAC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTATTGCAAAA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 GAGTTGAGAGAAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAAATCAAGAGATGGTT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AATGCGGTCCAAAGGAAGGGGGCTGTTGACCCGGGATAAAGATAGGAAGAAGGAGAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GCGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 GITGAAGCCAAAGGAAGAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATAAAAAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 153.6; DB 10; Length
Pred. No. 4.2e-21;
0; Mismatches 259; Indels
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DNA fragment encoding a wheat E2F-dimerisation partner (DP) protein.

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altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell ceath, lethality when overexpressed, altered necrosis patterns, increased plants increased blomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed protein content, increased anthocyanin levels, and altered leaf prenyl lipid content, increased anthocyanin levels, and content not form part of the printed specification, but was obtained in clectronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 ATCAGAAACAATATGATGAGAAGAACATCAGAGGACGAGGTCTAGGATGCTCTGAACGTAC 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1153 BP; 337 A; 225 C; 267 G; 324 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.1%; Score 153.4; DB 12; Length 55.1%; Pred. No. 4.5e-21; ive 0; Mismatches 271; Indels
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nes 354; Conservative
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AAPB0146-50 represent DNA fragments of a gene encoding a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly organ or tissue size
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                                    E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 6, 2005, 12:47:57; Search time 4249 Seconds (without alignments) 9755.705 Million cell updates/sec Run on:

US-10-088-830-1 1089 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10:0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST: \*
1: 9D estl: \*
3: 9D btc: \*
3: 9D btc: \*
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6: 9D est5: \*
7: 9D est5: \*
9: 9D gss1: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	CD882927 F1.111L02	CA764996 AF53-RDE	CD892664 G118.121J	BE456002 HVSMEG001	CR289243 CR289243	CL959517 OBIFCC003	CA078334 SCRLAM100	BE511883 946064A10	CF484481 POL1 25 C	CR286882 CR286882	BI802607 H084D10 E	CL909692 OA ABA000	CK278661 EST724739	BX831191 Arabidops	BX831357 Arabidops	BX831265 Arabidops	CA290160 SCAGFL801	AY108383 Zea mays	BX680618 BX680618	CL618454 OR BBa001	CL773898 OR_BBa008	CL773941 OR_BBa008	CL838498 OR_CBa006	CN215980 29828 Sus
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## ALIGNMENTS

RESULT 1 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	CD882927 F1.111L02F010430 F1 Triticum aestivum CDNA clone F111L02, mRNA sequence. CD882927 CD882927 CD882927 Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (bread wheat)
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Contact: Richard Bruskiewich
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International Rice Information System (IRIS;
International Rice Information System (IRIS;
http://www.iris.irri.org): D0201826
Assignment of putative function to the sequence |
Munich Information Center for Protein Sequences (http://mips.gsf.de)
Internation(Ocolumn: 03.
Location/Qualifiers
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Brnett, J. Arumugam, K., Lafitte, R., Wen
Brusklewich, R.M.
IRRI Drought, Stress Panicle cDNA Library
Unpublished (2002)
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International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
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/ organism="Oryza sativa (indica cultivar-group)"
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/ cultivar="IR64"
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/ tissue_Type="Panicles"
/ tissue_Type="Panicles"
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/ clone= lib="IRRI Drought Stress Panicle Library"
/ clone= lib="IRRI Drought Stress Panicle Library"
/ note="Vector: pBluescript II SK+; Water stress was
applied by not watering for 4 consecutive days. Panicles
were collected from control (well watered) and stressed
plants at 2 days before heading, at heading, 50% flowering
and 4 days after 50% flowering."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGAAAAACAGTTTGATGATCTCCCAAACATCAAGTTACGTAACCAAACACTGGAAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                           ch 38.7%; Score 421.6; DB 6; Il Similarity 77.1%; Pred. No. 2.2e-81; 581; Conservative 0; Mismatches 153;
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Best Local S:
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34.6%; Score 376.4; DB 2; Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 864 656 7288
Fax: 864 656 4293
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                 CD892664 14-JUL-2003 454 bp mRNA linear EST 14-JUL-2003 G118.121J23F010725 G118 Triticum aestivum cDNA clone G118121J23,
                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
(Dasee 1 to 454)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 TTGCATGATGTCTCTCAATCCTTGAGGGGATAAGGCGTAACAGCATAGGAAGAGCTGGC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 GGTTATGGCATCCGCCTTCCATTCGTACTGGTCAAGACATCTAGGAAAGCAAGGGTGGAA 70
                                                                                                                                                                                                                                                                                                                                                                                   This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
                                                                                                                                                                                                                                                        Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGCCACCCTTCACTAGAGACTCAAGAATATTACAAATGAATTAAAAAG-TGTTAGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4565"
/clone=#11811.023"
pollisaue_type="grain (118 degrees per day after
pollination)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.2%; Score 394.2; DB 6; Length 454; Best Local Similarity 96.7%; Pred. No. 2e-75; Matches 413; Conservative 0; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
                                                                                                                           Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="recital"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="G118"
                                                                                      CD892664.1 GI:32663198
                                                                                                                                                                                                                                                                                           Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .454
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

E (Doaes T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,

Fenton,R.D., Close,S.J., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library

Unpublished (2001)

On Jul 26, 2000 this sequence version replaced gi:13155022.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University
BE456002 607 bp mRNA linear EST 22-OCT-2001
HVSMEg0019D17f Hordeum vulgare pre-anthesis spike EST library
HVcDNA0008 (white to yellow anther) Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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                                                                       cDNA clone HVSMEg0019D17f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Total hq bases = 141
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 585.
Location/Qualifiers
                                                                                                                       BE456002.3 GI:16318905
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766 TAACAGCATAGGA 778
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B) Oryza sativa cDNA clone
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Oryza sativa
Oryza sativa
Cryza sativa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                      Gaps
                      7;
Pred. No. 1.5e-71;
0; Mismatches 56; Indels
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Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233,
Email: bhan@ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR289243 Oryza sativa library (Han ) p704410p5, mRNA sequence.
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/mol_type="mRNA"
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This is rice cdna est clone
Web site: http://www.ncgr.ac.cn.
Location/Qualifiers
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11 Similarity 87.9%;
457; Conservative
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Best Local
Matches 45
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AUTHORS
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CL959517

OBIFCC003026 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL959517

GSS 21-SEP-2004

OBIFCC003026 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL959517.1 GI:52373702

GSS.
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                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 ATCTAGGAAAGCAAGGGTGGAAATTGAGATTTCAGATGACTCGAAGTTTGCCCATTTCGA
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                                                                                                                                                                                                                    286 TGCAGACGAAATTTATTCAGAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGATGA
                                                                                                                                                                                                                                     61 TGCCGATAAGATTTTTGCGGAGCTGAAGTCCATTACGCAGAACGGTCTGGAGTTTGATGA
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                                                                                                                                                  226 GTACAGCAAAATAGTTTGTGAAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGT
                                                                                                                                                                                   1 GTTCAGCAAGATACTTTCTAAGAAGTTGAGGCCAAAGGAAGAACCACATATAATGAGGT
                                                                                                                    Gaps
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                                                                                Length 612;
/db_xref="taxon:4530"
/clone="p704a10p5"
/clone_lib="Oryza sativa library (Han B)
                                                                                                                    Indels
                                                                                Query Match
34.3%; Score 373.8; DB 7;
Best Local Similarity 79.7%; Pred. No. 5.7e-71;
Matches 441; Conservative 0; Mismatches 112;
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                                                                                       /organism="Oryza sativa (indica cultivar-group)"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic py46"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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                                                                                                                                                                                                                                                                                                      33.8%; Score 368.2; DB 9; Length 1119; 78.8%; Pred. No. 1e-69;
Chinese Academy of Sciences, Beijing 101300, China
                                                                                                                                                                                                                                                                                                                                              0; Mismatches 118; Indels
                Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
                                                                                            Class: exon-trapped.
Location/Qualifiers
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                                                                             Rice genomic sequence.
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Matches 439; Conservative
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VERSION
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CA078334
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/ Mod_ type="mRNA"

/ Ab xref="taxon:4547"

/ Ab xref="Taxon:4547"

/ Alone="GCRLAM1006A02"

/ Lone="GCRLAM1006A02"

/ Lone="SAN1"

/ Lone="Ib="AM1"

/ Lone="Ib="AM1"

/ Lone="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSportl; Site_1: Sal1; Site_2:

Mot!; An unidirectional CDNA library generated from [Apical meristem and tissues surrounding of mature plants! cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                     Control of Biologia Molecular e Engenharia Genetica
Control of Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1139
Fax: 55 19 3788 1108
Fax: 55 19 3788 1089
Email: parrudaeunicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at thttp://www.bccenter.fcav.unesp.br
Plate: 006 row: A column: 02
Seq primer: T7 Promoter Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 ccecrrccrearceccaagcercaececarieceeceaeagagagagagagagagargar
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                         and Arruda, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Saccharum officinarum"
                            Kemper, E.L.
               Vettore, A. L., da Silva, P. R., Kemper, E. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001) Contact: Arruda P
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(bases 1 to 665)
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Sorghum bicolor (sorghum)
SM Sorghum bicolor
Eukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
E (bases 1 to 634)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R.; Eastman, A. and Pratt, L.H.
An EST database from Sorghum: pollen
Lupublished (2003)
Contact: Cordonnier-Pratt NM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
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/mol type="mRNA"
/cullivar="BTx623"
/db xref="taxon:4558"
/clone="Poll_125 C08 A002"
/lab host="Dil0="T1" phage-resistant E. coli"
/lab host="Dil0="T1" phage-resistant E. coli"
/clone lib="Pollen; Vector: pME185-FL3; Site 1: Xho1;
/clone lib="Pollen; Vector: pME185-FL3; Site 1: Xho1;
/note="Organ: Pollen; Vector: pME185-FL3; Site 1: Xho1;
Site 2: Xho1; The library was prepared from poly4+ RNA
from pollen at the late vacuolated-vacuolated stage of
development. Pollen was harvested from greenhouse-grown
panicles of sorghum line BTx623. Panicles were removed
from the flag leaf prior to emergence, when no detectable
amylase is present in pollen of male-fertile lines. This
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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genter, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                                                                                                                                                                                                                               404 ATTGCAAAAGAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAA 463
                                                                                                                                                                                                                                                                                                                              375 ATCACAAAAGATGAAAAAGAGATAAAATGGATGGGCTTGTCTAATTTCCAATATGAAAAG 434
                                                                                                                                                                                                                                                                                                                                                                                          464 ATABAGAAGCTTGAAGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCA 523
GTTGCAGACGAAATTTATTCAGAGCTGAAGTCCATGGCACATATTGGTCAAGGGTTTGAT
                                                                                                             258 GTTGCAGATGAAATTTGTGGAGGCTGAAGT----TGACTCTTATTGGTCAAGAGTTTGAT
                                                                                                                                                                 344 GAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTT
                                                                                                                                                                                                 315 GAGAAGAATATCAGGAGGAGGAGTGTATGATGCTTTTAATGTGCTAATTGCACTACGTGTT
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POLI_25_C08.gl_A002 Pollen Sorghum bicolor cDNA clone
POLI_25_C08_A002 5', mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
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                               521 GCACTCCTCCAGGAAATCGAAAAACAGTTTGATGATCCCCAAAACATCAAGTTACGTAAC 580
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

(Dases 1 to 548)

Walbot,V.

Malbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                   561 AAACTTCTCCAGAAAATTGAACGACAGGTTGATGACCTTCAGAATATCAAGTTCGGCAAC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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lab"
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                                                                                                                                                624
                                                                                                                                                                                                    621 CAGTTACTACAGAAGGCCAGCAAAGAGTGCGAATGGGATCAGCCT
                                                                                                                                                CAAACACTGGA-AAGCTCAGCAGAGAATGTTAATGGCATCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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to 3 Kb with a 1 Kb average."
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Location/Qualifiers
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Stanford University
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/tissue_type="tassels"
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/cultivar="OH43"
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CR268682 Oryza sativa library (Han B) Oryza sativa cDNA clone
p730d01p5, mRNA sequence.
CR286882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryzae.

1 (bases 1 to 702)
Han, B., Feng, Q., Huang, Y.C., Ying, K., Li, Y., Guan, J.P., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, L., La, Y.C., Li, T., Zhang, Y., Hu, H., Jia, P.X., Zhang, L., Lan, L. E., Chen, W., Wu, S.A. and Xue, Y.B.
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                                                                        CDNA
stage represents pollen collected from anthers about 8-1 days prior to anthesis. Double-stranded cDNA was cloned uniditectionally into different Draili sites of the pME185-FL3 vector (-prime Draili site is CACTGTGT, 3-prime Draili site is CACTGTGT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 --CTGACTCTTATTGGTCAAGAGTTTGATGAGAATATCAGGAGGAGAGTGTATGATG
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                                                                                                                                                                                                                                                                                                    152 TCAGCGAAGGAGCCGGGCTCCCTCCGCTTCCTCCTGGACGGGAAGCGTCGGCGGCAATG
                                                                                                                                                                                                                                                                                                                                    CGGTCCAAAGGAAGGGGCTGTTGACCCCGGATAAAGATAGGAAGAAGAAGGCTGCGG
                                                                                                                                                                                                                                                                                                                                                                       CACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACTACAAAAAAATAGTTTGTGAGAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCAGCGGATCGCCGGGGGGCCTTCGCGAGTTCAGCAAGATAGTTTCTAAAAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCCAAAGGAAGAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AGAGCAAAGGACGGACTACTTACAATGAGGTTGCAGATGAAATTTGTGGGGAGCTGAAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 CCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 TCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTTTGATG
                                                                                                                                                                                                     CCGCAATGGCCCCTCCCCGCGCGGGCTGCTGCGGCCGCTACCGCCGCACTGGACCTGA
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9
                                                                                                                                    Score 264.2; DB 7; Length 634;
Pred. No. 4.7e-47;
0; Mismatches 158; Indels. 6
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                                                                                                                                    24.3%;
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Oryza sativa
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Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 AIGCITIC-AIGIGCICATIGCAATICGIGITATIGCAAAAGATAAAAAGGATAIAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAA-AAACAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATGATCTCCAAAACATCAAGTTACG-TAACCAAACACTGGAAAGCTCAGCAGAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 TGATGACCTTCAGAATATTACATTAAGCAAACCAGGCTAGTACGAGGCCAGGACAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609 TTAATGGCATCC--GCCTTCCATTCGTATTGGTCAAGACA--TCTAGGAAAGCAAGGGTG
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H084D10 Endosperm library from Oryza sativa (10 days after anthesis) Oryza sativa cDNA clone H084D10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                     702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 CGGCACCGAGGATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGT
                                                                                                                                                                                                                                                                                                                    (Han B) "
                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                 1. .702.
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="p730d01p5"
/clone_lib="Oryza sativa library
                                                                                                                                                                                                                                                                                                                                                                                   Score 237.8; DB 7;
Pred. No. 2.7e-41;
0; Mismatches 112;
                                                                      China
Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 20233, Ch
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cdna est clone
Web site: http://www.ncgr.ac.cn
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BI802607.1 GI:16575311
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.8%;
Best Local Similarity 75.7%;
Matches 373; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 CATTCACCCTTAAGAGGCACAAGAATGTGACAAACCATTGAAGTGTCAAAACTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCACAGCCGGATTCTTTTGCACAGCTATGTATAGCTATA-----TATCCTCATGAAAA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 GCACCACCAGTTTCTTTTGCACAGTTATGTATAGCTATAGCGTACCTTTCAGTATGGAAA 359
                                                                                                                                                                                                                                                                                               /tissue_type="Endosperm"
/dev_stage="10 days after anthesis"
/clone_lib="adosperm library from Oryza sativa (10 days after anthesis)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACCTTCCAGAATATACATTACGCAACCAGGCTAGTCAGAGGCCA-CAGAAAGTGTTAAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 GATCTCCAAAACATCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCCTTCACT-AGAGACTCAAGAATATTACAAATGAATTAAAAGTG----TTAGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 CTCGACCTAGTTTATAGGACAGTCTCTCAGGCTTTTTAGCAGATATGACCTGCGAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 TTATGTATAAACTCATTGCCGTTTCAATTCGAAGCTTGTGTACAAGCTCCATTGATGAAA
Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.X. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                Email: webmaster@estarray.org, URL: http://www.estarray.org
Seq primer: M13 forward primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 218; DB 4; Length 548;
Pred. No. 5.6e-37;
0; Mismatches 140; Indels
                                                                                                      Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
                                                                      Contact: Haitao Dong, Debao Li
Bioinfomatics and Gene Network Research Group
                                                                                                                                                                                                                 1. .548
/organism="Oryza sativa"
/mol_type="mxxx"
/db xref="taxon:4530"
/clone="H084D10"
                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pSport2"
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.0%;
Best Local Similarity 71.1%;
Matches 391; Conservative
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                                      TITLE
JOURNAL
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GSS 14-SEP-2004

linear

DNA

836 bp

CL909692

RESULT 12 CL909692/c LOCUS

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/clone="OA_ABAG009114"
/tissue_type="young leaves"
/tissue_type="young leaves"
/tispue_type="young leaves"
/clone lib="OA_ABa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CK278661 BST724739 potato abiotic stress cDNA library Solanum tuberosum cDNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 836)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 CCATTCAGTAATGAAAACTCGACCTAGTTTATAGGACAGTATCTCAGGCTTTTAAACAAA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714 GIGCACCATICACATIGCATGATGATCTCTCAATCCTTGAGGGGGTAAGGCGTAACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 GIGCACCATICACCAIGCAIGAIGAIGAICTCAAICCITGAAGCCAICAGGCGIAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 774 TAGGAAGAGCTGGCCGCCCCCCTTCACT--AGAGACTCAAGAATATTACAAATGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 14; Gaps
OA ABa0009114.f OA ABa Oryza australiensis genomic clone OA ABa0009114 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                    OMAP Project
Unpublished (2004)
Unpublished (2004)
Unpublished (2004)
Arizona Genomics Institute
Arizona Genomics Institute
Forbes Building Room 303, Tucson, AZ 85721-0036, US:
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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74.8%; Pred. No. 1.9e-24;
iive 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza australiensis"
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Plate: 0009 row: I column: 14
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: TAA TAC GAC TCA CTA TAG
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/db xref="taxon:4532"
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j. .836
                                                  CL509692
CL909692.1 GI:52018571
GSS.
                                                                                                                                Oryza australiensis
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Best Local Similarity 74.8
Matches 246; Conservative
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DEFINITION
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506

995

527 683 587

647

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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( Chases I to 1403)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Craudd, C., Quetier, F., Scarpelli, C., Schachter, V.,
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
  228 ATCAGAAACATATGATGAGAAGAACATCAGACGACGAGTCTACGATGCTCTGAACGTAC 287
                                                                                                                                            288 TTÄTGGCTATGGATATCATTTCTAAAGATAAAAGGAAATACAGTGGAAGGGATTACCAC 347
                                                                                                                                                                                                                                                        348 GCACTGATGCAAATGATATTGAGGAGCTAAAGACTGAGCGTCTTAACTTGAGAAATAGGA 407
                                                                                                                                                                                                                                                                                                                                                                    408 TIGAAAAGAAAGCAGCCIAITIAGAAGAACTIGAAGAICAATAIGIAGGGCTICAAAACC 467
                                                                                                                                                                                                                                                                                                                                                                                                                           567 TCAAGTTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTA---ATGGCATCCGCC 623
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castel V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Welssenbach J., Salanoubat M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 TCATAAAACGCAATGATCAGTTGTATGGCTCAGGCAATGCTCCTAGTGGTGTGTGGCCTT
                                                                                                                                                                                                                                                                                                            TTAGGAACAAGAAGGCACTCCTCCAGGAAATCGAAAAACAGTTTGATGATCTCCCAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 TACCGTTTATTTTAGTGCAGACTCGTCCTCATGCAACAGTTGAAGTGGAAATATCAGAAG
                                                                                                                                                                                                447 ATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 ATATGCAGCTGCATTTCGACTTCAACAGCACTCCGTTTGAGCTACATGACGATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAATTGAGATTTCAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana Full length cDNA Complete sequence GSLTLS67ZA12 of Adult vegetative tissue of strain col-0 Arabidopsis thaliana (thale cress).
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Arabidopsīs thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     744 CAATCCTTGAGG 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /done_lib="potento abiotic stress cDNA library"
/done_lib="potento abiotic stress cDNA library"
/note="Vector: DCNVSport6.1; Site_1: ECORI; Site_2: NotI;
supplier: Solanum tibersoum var. Kennebec plants were
grown from cuttings on a l6hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mm Nacl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; rocfe:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; rochs:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and rocts were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed rocts were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the CDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="abiotic stress treated leaf and root tissue"
|lab_host="DH10B-TonA"
                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots, steride; lamides, Solanales; Solanaceae; Solanum.

1 (bases 1 to 992)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AGGTIGCIGATGAACTIGIAGCIGAGITITCIGAIGCIACCAATAGIGTIGCAGGCCCAG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGATAAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGATCACCGGTTGGGGGCTCC
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Pred. No. 9.9e-23;
0; Mismatches 252; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Solanum tuberosum"
clone POAE738 5' end, mRNA sequence
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castel V. Aury J.M., Jailon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. Montation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences): 5 prime and 3 prime are assembled with Phrap.
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		1456 6, Application US/09023655 5607879 FORMATION: T. Cocke, Benjamin G. T. Susan G. Stuart T. Susan G. Stuart T. Jeffrey J. Seilhamer T. Jeffrey J. Seilhamer T. Jeffrey J. Seilhamer T. JOHNER DRESSION T. SEQUENCES: 1508 TOWENTION: COMPOSITION FOR TH INVENTION: EXPRESSION TATA TATA TATA TATA TATA TATE: PLOPPY disk TREADABLE FORM: TYPE: PLOPPY disk TREADABLE FORM: TATON NUMBER: US/09/023,655 DATE: TCATION: TATON NUMBER: DATE: TCATION: TATON NUMBER: PA-0001 US TREADATION: TATON NUMBER: PA-0001 US TREADATION: TATON NUMBER: PA-0001 US TREADATION NUMBER: PA-0001	
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622 622 622 623 623 633		RESULT 1  US-09-023-655-1456  Sequence 1456, Application US/09023655  Patent No. 6607879  GENERAL INFORMATION: APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer ITILE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICAL STREET: 3174 PORTER DRIVE COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA CONFUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: BM PC COMPATION OF PRICATION UNMBER: US/09/023,65 STATE: CALIFORNION DATA: APPLICATION NUMBER: US/09/023,65 FILING DATE: CLASSIFICATION NUMBER: BA-0001 FRIEDRA APPLICATION NUMBER: BA-0001 FRIEDRA APPLICATION NUMBER: BA-0001 FRIEDRA APPLICATION NUMBER: TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUMBER: BA-0001 TELECOMMUNICATION NUM	Query Match
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239 GTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT 298
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467 AAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTC 526
                                                                         699 CAGAATCTGGAGATAGAGAAGCAGAGGGGGATAGAACGGATAAAGCAGAAGCGGGCCCAG 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: detaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                          527 CICCAGGAAATCGAAAAAAGTTTGATGATCTCCAAAACAT 567
                                                                                                                                                                                                                                   759 chgcaagaachrcrccracaaarccchrhcaaaacch 799
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COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
REGISTRATION NUMBER: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTAWOOM, ATTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/POCKET NUMBER: 117-220
TELEPHONE: 703-816.4000
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56.0%; Pred. No. 7.6e-12;
iive 0; Mismatches 138;
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STREET: 1100 No. 5859199th Glebe Rd.
CITY: Arlington
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Patent No. 5859199
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 191; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION:
US-08-723-415B-5
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US-09-649-016-3349
i Gequence 1349, Application US/09949016
f Requence 1349, Application US/09949016
f Requence 1349, Application US/09949016
f RENEAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILER REFERENCE: CL001307 PILER REFERENCE: CL001307 PILO APPLICATION NUMBER: US/09/949,016
f CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR PRILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
FRIOR TOWNERS FASTSEQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                    296 ATTTATTCAGAGCTG-----AAGTCCATGGCACATATTGGTCAAGGGTTTGAT 343
                                                                                                                                                                                                                                                                                                                                                             429 CTGGTGTCAGAGTTCACCAATTCAAATAACCATTTGGCTGCTGATTCGCAGGCTTATGAT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                          344 GAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTT 403
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                                                                                                                         236 ATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 ATTGCAAAAGAAAAAAGGAGATACGGTGGATGGGCCTTTCAAATTACAGATATGAAAAA
                                                Gaps
                                                12;
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                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 524 CTCCTCCAGGAAATCGAAAAACAGTTTGATGATCTCCCAAAACAT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 CAGCIGCAAGAACTICTCCTACAGCAAATCGCTTICAAAAACCT 712
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Pred. No. 1.6e-14;
0; Mismatches 135; Indels
        Pred. No. 6.8e-15;
0; Mismatches 132;
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        Best Local Similarity 58.1%;
Matches 200; Conservative
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Best Local Similarity 57.8
Matches 197; Conservative
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ORGANISM: Human
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us-10-088-830-1.rni

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TYPE: DNA
ORGANISM: mouse
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US-09-640-211A-566
                                                                                                                                                                                                                                                                                                          LENGTH: 1157
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                                   364 TCAAAGGAAAAAAAAAAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGC 423
                                                                             467 AAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGACCTC 526
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                                                                                                                 244 GTATCTGAGTTTACCAACTCAAATAACCATCTGGCAGCTGATTCGCAGGCTTATGATCAG 303
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APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
TITLE OF INVENTYON: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1157
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Pred. No. 7.6e-12;
0; Mismatches 138; Indels 12;
                                                                                                                                                             CTCCAGGAAATCGAAAAACAGTTTGATGATCTCCAAAACAT 567
                                                                                                                                                                                                   484 CTACAAGAACTICICCTICAGCAAATIGCTITIAAAAACCI 524
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Patent No. 6159691
GENERAL INFORMATION:
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Best Local Similarity 56.0%;
Matches 191; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1)..(1110)
US-09-189-627A-5
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                                                                                                                                                                                                                                                           RESULT 4
US-09-189-627A-5
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US-09-710-861-5; Sequence 5, Application US/09710861; Patent No. 6387649; GENERAL INFORMATION:

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239 GTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 TATTCAGAGCTGAAGTCCA-----TGGCACATATTGGTCAAGGGTTTGATGAG 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GTATCTGAGTTTACCAACTCAAATAACCATCTGGCAGCTGATTCGCAGGCTTATGATCAG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 TCAAAGGAAAAAAAAAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGC 423
APPLICANT: de la Luna, Susana;
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF;
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627
FRIOR APPLICATION NUMBER: US/09/189,627
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1998-11-10;
PRIOR PELING DATE: 1998-11-10;
PRIOR FILING DATE: 1996-09-30;
PRIOR FILING DATE: 1996-05-15;
NUMBER OF SEQ ID NOS: 25;
SOFTWARE: PATENTIN VOYEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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Sequence 566, Application US/09640211A

Betent No. 683346

GENERAL INFORMATION:

APPLICANT: Wood, Martion

APPLICANT: Shenk, Michael A.

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REPRENCE: 11000.1021C1U

CURRENT APPLICATION WOMBER: US/09/640,211A

CURRENT APPLICATION WOMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEC ID NOS: 2368

SOFTWARE: PESESEQ for Windows Version 4.0

SEQ ID NO 566

LENGTH: 358
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; ORGANISM: Pinus radiata
US-09-640-211A-566
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; LOCATION: (1)..(1110)
US-09-710-861-5
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490 AGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTCCAGGAAATGGAAAACAGTT 549
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                                                                   384 gaagaargecaaggecrecgecarrircrecargaaggrerergagaggrecagaggag
                                                                                                                                                                                                                      444 AddaAccaccricciAcaAridAcdricdcricAcdAcricGregCAGACricAcccca 503
                                                                                                                                                                                                                                                                                                                                                                             504 caaccacarreraccaaacgaarcagerrargaccagaagaacarcegegegegerere 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 CGATGCCTTAAATGTGCTAATGGCCATGAACATCATCTCCAAGGAGAAGAAGGAGATCAA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 GTGGATGGGCCTTTCAAATTACAGATATGAAAAAATAAAGAAGCTTGAGGAAGTTCGTAA 489
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202 GATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAA 261
                                                                                                                                                                                                                                                                                                         316 -----CATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTA
                                                                                                                                                      262 AGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08602846
Patent No. 5871901
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEINS.
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5871901th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1700;
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Pred. No. 5.1e-11;
0; Mismatches 163;
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TYPE: nucleic acid and encoded amino acids
STRANDEDNESS: double
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FILLING DATE: 26-FEB-122.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CRAMPORD, ARTHUR R.
REGISTRATION NUMBER: 52,327
REFERENCE/DOCKET NUMBER: 620-12
TELECOMMUNICATION INFORMATION:
TT. FORMATION: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0
CURRENT APPLICATION DATA:
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FILING DATE: 26-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 53.7%;
Matches 203; Conservative
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STATE: Virginia
COUNTRY: USA
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US-08-602-846-1
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US-08-602-846-1
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                                   7.8%; Score 85; DB 4; Length 358; 62.5%; Pred. No. 9.3e-12; ive 0; Mismatches 80; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08428131
; Patent No. 5863757
; GENERAL INFORMATION:
    TITLE OF INVENTION: Transcription Factor DP-1
; NUMBER OF SEQUENCES: 14
; CORRESPONDES: 14
; CORRESPONDES: 14
; CORRESPONDES: 15
; STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPRACE (703) 816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 ATGGGCCTTTCAA 446
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                                                                                                           Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1700 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY: CDS
, LOCATION: 55..1284
US-08-428-131-1
                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
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US-08-428-131-1
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                                                                         Score 83.2; DB 3; Length 1 Pred. No. 5.1e-11; 0; Mismatches 163; Indels
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Gene Transcription
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APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Grath, Annette
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Modification of Gene Tray
FILE REFERENCE: 11000.1021C1U
CURRENT PEPLICATION NUMBER: US/09/640,211A
CURRENT PELLING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 465
LENGTH: 364
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Patent No. 6833446
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                                                                      Query Match 7.6%;
Best Local Similarity 53.7%;
Matches 203; Conservative
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Best Local Similarity 57.9
Matches 175; Conservative
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LOCATION:
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US-09-078-596-1
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                                                                                                                                                                                                                                                                               504 CAACCACATTCTACCAAACGAATCAGCTTATGACCAGAAGAACATCCGGCGCGCGTGTCTA 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624 ATGGATCGGCCTGCCCACCAACTCAGCTCAGGAGTGCCAGAACTTAGAGGTGGAGAGGCA 683
                        GATCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAA
                                                                      384 GAAGAATGGCZAAGGGCCTGCGGCATTTCTCCATGAAGGTGTGTGAGAAGGTGCAGAGGTG
                                                                                                                                                                          444 AGGAACCACCTCCTACAATGAGGTGGCTGACGAGGTGGTGGCAGAGTTCAGCGCTGCCGA
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                                                                                                                         262 AGGAAGAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTGAAGTC----
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STATE: Virginia
COUNTR: Virginia
COUNTR: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
WEDIUM TYPE: FORM:
COMPUTER: Plan PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09078596
Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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470 AAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACTCCTC 529
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                                       304 AACATTAGACGAAGAGTTTATGATGCTTTAAATGTACTAATGGCGATGAACATAATTCA 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 AAGGAAAAAAAAAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGCCAG
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                                                                                        239 GTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TEAMSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF FILE REFERENCE: 620-54 ANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF FILE REFERENCE: 620-54 ANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF CURRENT APPLICATION NUMBER: 08/723,415 PRIOR FILING DATE: 1996-09-30 PRIOR FILING DATE: 1996-09-10 PRIOR PRIOR APPLICATION NUMBER: 69 9610195 PRIOR FILING DATE: 1996-05-15 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3 LENGTH: 1154
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                                                                                                                                                                                                                                                                                530 CAGGAAATCGAAAAACAGTTTGATGATCTCCAAAACAT 567
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350 AATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCAT
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APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
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Matches 186; Conservative
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US-09-189-627A-3
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FEATURE:
NAME/KEY: CDS
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US-09-189-627A-3
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                                            237 GCATTGAATGTACTGATGGCAATGGACATCATATCAAAGGACAAGAAGGAAATTCAGTGG 296
                                                                                                                                         297 AAGGGGTTACCTAGCACAAGTCCTAATGACCTTGAAGACTTGAAGGCAAAGCGCATGGGA 356
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81.2; DB 2; Length 1 Pred. No. 1.4e-10; 0; Mismatches 143; Indels
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COMPUTER: IBM PC compatible
ONDERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 15-MAY-1996
ATTONEY/AGENT INPORMATION:
NAME: CLAWFORM AT INPORMATION:
NAME: CLAWFORM AT INPORMATION:
NAME: CLAWFORM AT INPORMATION:
NAME: CLAWFORM AT INPORMATION:
TELEPHONE: 703-816-4100
TELEPHONE: 703-816-4100
                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08723415B
Patent No. 5859199
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7.5%;
Best Local Similarity 55.0%;
Matches 186; Conservative C
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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; LOCATION:
US-08-723-415B-3
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US-08-723-415B-3
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## Sequence 3, Application US/09710861
## Patent No. 6387649
## Patent No. 6387649
## Patent No. 6387649
## APPLICANT: La Thangue, Nicholas
## APPLICANT: de la Luna, Susana
## TILE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
## CURRENT APPLICATION NUMBER: US/09/710,861
## CURRENT APPLICATION NUMBER: US/09/10,861
## PRIOR PILING DATE: 1998-11-10
## PRIOR FILING DATE: 1998-11-10
## PRIOR PILING DATE: 1996-130
## PRIOR PILING DATE: 1996-130
## PRIOR PILING DATE: 1996-09-30
## PRIOR PILING DATE: 1996-09-30
## PRIOR PILING DATE: 1996-05-15
## NUMBER OF SEQ ID NOS: 25
## NUMBER OF SEQ ID NOS: 25
## NUMBER PATENTIN VET: 2.0
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Pred. No. 1.4e-10;
0; Mismatches 143; Indels 9
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Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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STREET: 1100 No. 5859199th Glebe Rd.
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Matches 186; Conservative
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LOCATION: (1)..(1107)
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LENGTH: 1154
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Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
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                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION 35
PRIOR APPLICATION NUMBER: US/08/723,415B
FILING DATE: 10-SEP-1996
ATPONENT/AGENT INPOMBER: EB 9610195.1
FILING DATE: 15-MAY-1996
ATPONENT/AGENT INPOMBER: 25,327
REFERENCE/DOCKET NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
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TELEFRAK: 703-816-4100
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                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.0%;
Matches 186; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-723-4158-7
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239 GITIGIGAGAAAGIIGAAGCCAAAGGAAGAACAACAIACAAIGAGGIIGCAGACGAAAII 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 TATTCAGAGCTGAAGTCCATGGCACATATT-----GGTCAAGGGTTTGATGAAAG 349
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                                                                                                                                                                                                                                                                                                      Query Match 7.5%; Score 81.2; DB 3; Length 1202; Best Local Similarity 55.0%; Pred. No. 1.4e-10; Matches 186; Conservative 0; Mismatches 143; Indels 9
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PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1202
                                                                                                                                                   ; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
US-09-189-627A-7
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Search completed: February 6, 2005, 13:09:14 Job time : 230 secs

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February 6, 2005, 13:09:21; Search time 690 Seconds (without alignments) 9084.062 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/US06 PUBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06 PUBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06 PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06 PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1089
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	Match	Query e Match Length DB I	B	ID	Description	
1 0	452.6	41.6	1406	18	US-10-437-963-33888	Sequence 33888, A	
7	385.4	35.4		18	US-10-425-115-4115	Sequence 4115, Ap	
m	203.4	18.7	476	18	US-10-767-701-17642	Sequence 17642, A	
4	150.8	13.8		18	US-10-739-930-1190		
S	141.6	13.0	•	11	US-10-424-599-43806	Sequence 43806, A	
ø	139.8	12.8	_	18	US-10-425-115-87351	Sequence 87351, A.	
7	133.4	12.2	•	18	US-10-425-115-2033	Sequence 2033, Ap	
ω	131.8	12.1	-	17	US-10-425-114-4049	Sequence 4049, Ap	
σ	124.6	11.4		17	US-10-425-114-20051	Sequence 20051, A	
10	121.4	11.1	1751	17	US-10-424-599-43105	Sequence 43105, A	
17	120	11.0		17	US-10-425-114-36537	Sequence 36537, A	

Sequence 6106, Ap	101	ø	1176, 7	3,		63675,	8, Appl	Sequence 64593, A	Sequence 566, App	Sequence 465, App	Sequence 91931, A	Sequence 21, Appl	edue	Sequence 4, Appli	Sequence 1357, Ap	Sequence 1399, Ap	Sequence 73, Appl	Sequence 569, App	Sequence 13784, A	Sequence 13317, A	Sequence 11218, A	Sequence 178785,	, Appli	5594	8671	19,	69	69	648,	648,	Sequence 293, App	equence 5013	Sequence 118211,
US-10-767-795	US-10-198	US-10-641-643	-954-456-11	US-10-357-930-20	US-10-357-	US-10-437-963-63	2	63	9	9	-66	5	US-10-172-118-	7 US-10-160-554-4	/ US-10-342-887-1357	43-139	ns	US-10-106-698-56	78	US-10-424-599-133	US-09-960-352-11218	US-10-425-11	US-09-811-367B-6	US-10-425-115-5	US-10-021-323-86	US-10-821-273-1	Þ	US-10-182-936A-69	US-10-477-	US-10-680-287A-64	US-10-723-860-293	US-10-723-860-501	3 US-10-425-115-118211
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## ALIGNMENTS

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TYPE: DNA
ORGANISM: Zea mays
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US-10-767-701-17642
                                                                                  US-10-425-115-4115
SEQ ID NO 4115
              LENGTH: 774
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US-10-425-115
is Sequence 4115, Application US/10425115
is Sequence 4115, Application US/10425115
is Definited and Control of US20040214272A1
is GENERAL INFORMATION:
is APPLICANT: Las Rosa, Thomas J.
is APPLICANT: Zhou, Yihua
is APPLICANT: Zhou, Yihua
is APPLICANT: Zhou, Yihua
is APPLICANT: Consider of US APPLICANT: Consider of US APPLICANT: Consider of US APPLICANT: Consider of US APPLICANT: Consider of US APPLICANT: US YI (13322) B
is FILE REFRENCE: 38-21 (53222) B
is CURRENT FILING DATE: 2003-428
is UNMBER OF SEQ ID NOS: 369326
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              CTGAAGTCCATGGCACATATTGGTCAAGGGTTTTGATGAGAAGAATATTAGGCGGAGAGTG
                                CTGAAGTCCATTACGCAGAACGGTCTGGAGTTTGATGAGAAGAATATTAGGCGGAGGGTA
                                                                  TATGATGCTTTCAATGTGCTCATTCCAATTCGTGTTATTGCAAAAGATAAAAAGGAGATA
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                                                                                                                                                                                                774;
                                                                                                                                                                                                     DB 18; Length
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                      Score 385.4; DB 18;
Pred. No. 3.2e-82;
0; Mismatches 176;
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_103754C.1
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTAACAGCATAGGAAGA 781
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Best Local Similarity 74.0%;
Matches 547; Conservative
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBNE: 38-21(33223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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     547 CTGGAAGAGGACTACGTCAATTTAGTATGAAAGTTTGTGAAAAGGTGGAAAGCAAAGGAA 606
                                                                                                                                                                                                                                                                                                                                                              432 GGATGGGCCTTTCAAATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAG 491
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                                                                                                         607 GGACAACTTACAATGAGGTTGCAGACGAGCTTGTTGCTGAATTTGCACTTCCAAATAACG
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                                                                                                                                                           312 AGTCCATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATG
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                                                          267 GAACAACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCT
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US-10-424-599-43806
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Pred. No. 1.5e-23;
0; Mismatches 259;
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Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.5%;
Matches 345; Conservative
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICAD DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 17642
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Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION:
PLEATE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 9.9e-26;
0; Mismatches 262; Indels 18;
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                                                                                                                                                                                                                                                                                                                                                            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                              61; Indels
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US-10-739-930-1190
                                                                                                                                                                                                                                                                                                                                                         Query Match
18.7%; Score 203.4; DB 18;
Best Local Similarity 79.7%; Pred. No. 1.3e-38;
Matches 240; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: LIB3476-039-P1-K1-D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.3%;
Matches 346; Conservative
                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                         US-10-767-701-17642
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                                                                                                                                                                              LENGTH: 476
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Sequence 2013, Application US/10425115

| Sequence 2013, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Zhou, Yihua
| APPLICANT: Zhou, Yihua
| APPLICANT: Caro, Yongwid:
| APPLICANT: Caro, Yongwid:
| APPLICANT: Caro, Yongwid:
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                                                                                                                                                                                                       254 AGGCACCAGATCCTGATAACCCTAACGCGCAACAATATGATGAGAAAATATACGACGAA 313
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                                                                         DB 18; Length 1483;
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Best Local Similarity 51.4%; Pred. No. 1.4e-21;
Matches 385; Conservative 0; Mismatches 331;
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US-10-425-115-2033
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FUDILICATION No. US20040214272A1
GENERAL INFORMATION: US20040214272A1
GENERAL INFORMATION: Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
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                                                                                                                                                                               425 TIGCCCCTGATCAGCAACAATATGATGAAAAAAAACATCCGCCGAAGGGTCTATGATGCT
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                                                                                                                       ATGGCACATATTGGTCAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCT
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12.8%; Score 139.8; DB 18; Length
Best Local Similarity 55.1%; Pred. No. 4.3e-23;
Matches 338; Conservative 0; Mismatches 242; Indels
272 ACATACAATGAGGTTGCAGACGAAATTTATTCAGAGCTG
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; OTHER INFORMATION: Clone ID: MRT4577_179669C.1
US-10-425-115-87351
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ORGANISM: Zea mays
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US-10-425-115-87351
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115 GCGAGAGCACCGTCGCCGCCTAAACGGACTTGACCCCCACGGCGACGACGCTCCAT 174
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   CGCCTCCCCCCCGCGGGGGCTGCGGCCGCTACCGCCGCCACTGGACCTGACCGGCGTGC 83
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                                                                                                                                             144 GGAAGGGGGCTGTTGACCCGGATAAGATAGGAAGAAGGAGAAGGCTGCGGCACCGAGGA
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Publication No. US20040034888A1
GENERAL INFORMATION:
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Scorelic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
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CURRENT APPLICATION WUNDER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                  TCACCGGTTGGGGGCTCCGCGAGTACAGCAAAATAGTTTGTGAGAAAGTTGAAGCCAAAG
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OTHER INFORMATION: Clone ID: 700347688_FLI
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US-10-425-114-4049
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Sequence 36537, Application US/10425114

Sequence 36537, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Soreen, Yuhua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska Jack E
APPLICANT: Tabaska Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5313) B
CURRENT FILING DATE: 2003-04-28

UNMBER OF SEQ ID NOS: 73128

SEQ ID NO 36537

LENTH: 911
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                                             332 CAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATT
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US-10-425-114-36537
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ORGANISM: Zea mays subsp. mexicana
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Best Local Similarity 55.2
Matches 256; Conservative
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APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 CAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACGTAACCAAACACTGGAAAGCTCAGCAGAGAATGTTAAT---GGCATCCGCCTTCCA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICGIATIGGICAAGACAICTAGGAAAGCAAGGGIGGAAATIGAGAITTCAGAIGACCICG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTITGCCCATTCGAGTTCAATGGTGCACCATTCACATTGCATGATGATCTCTCAATC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 calcuricacarurucaruricaaraccacuccurusagericarigaricaracuarum 692
                                                                                                                                                                                                                                                                                                    332 CAAGGGTTTGATGAGAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATT 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACTICGIGITATIGCAAAAGAAAAAAGGAGAIACGGIGGAIGGGCCTITCAAATTAC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 GCAATGGATATTATTTCTAAGGATAAAAAGGAAATTCAATGGAAGGGTCTCCCTCGTACT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 AGTCTAAGCGATÁTTGAAGÁGCTAAAGTCGGAGCGTCTTGGGCTAAGGAATAGAATTGAA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAAGAAGGCACTCCAGGAAATCGAAAAACAGTTTGATGATCTCCAAAAACATCAAG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caaceaaareaecaactararaceceaaaarececeaareeaageaecererreece 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagaaagcagccrarrigcaagagcrgaaggaggaaracaraggrcrrcagaaacrrara
                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                          Length 1167;
                                                                                                                                                                   Score 124.6; DB 17; Length
Pred. No. 1.7e-19;
0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1%; Score 121.4; DB 17; 56.9%; Pred. No. 1.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_138923C.1
US-10-424-599-43105
                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-045-C12_FLI
US-10-425-114-20051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 43105, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                       Query Match
Best Local Similarity 57.4%;
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56.9
Matches 243; Conservative
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ORGANISM: Glycine
      ORGANISM: Glycine
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403 AAAGTGTGTGAGAAAGTTCAACGAAAAGGTACAACATCGTACAATGAAGTCGCTGATGAG 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 GAAGAATATTAGGCGGAGAGTGTATGATGCTTTCAACGTTCTCATTGCACTTCGTGTTAT 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 TCAGAATCTGGAGATAGAAAGCAGAGGCGGATAGAACGGATAAAGCAGAAGCGGGCCCA 702
                                                                                                           APPLICANT: Lillie, James
APPLICANT: Mangy Youchny
APPLICANT: Wangy Youchny
APPLICANT: Wangy Youchny
APPLICANT: Wangy Youchny
APPLICANT: Wangy Youchny
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 2968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 ATAGTTTGTGAGAAAGTTGAAGCCAAAGGAAGAACAACATACAATGAGGTTGCAGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 CTGGTGTCAGAGTTCACCAATTCAAATAACCATTTGGCTGCTGATTCGGGCTTATGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 AAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTCAACAAGATTAGGAACAAGAAGGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.1%; Score 99.2; DB 14;
58.2%; Pred. No. 3.2e-13;
iive 0; Mismatches 133;
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1455, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
                             Sequence 10136, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1, 2
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.2
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
     JS-10-198-846-10136
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Sequence 6106, Application US/10767795

Sequence 6106, Application US/10767795

Publication No. US20040181830A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53534)B

CURRENT APPLICATION NUMBER: US/10/767,795

CURRENT APPLICATION NUMBER: US/10/767,795

NUMBER OF SEQ ID NOS: 117596

SEQUENCE OF SEQ ID NOS: 117596
TTACGTAACCAAACACTGGAAAGCTCAGCAGA---GAATGTTAATGGCATCCGCCTTCCA 628
                                                  241 CAACGAAATGAGCAATCATATGCTTCAGGAAACACGCCTTCTGGTGGAGTGGCTTTGCCA 300
                                                                                                                                                                                                                          689 AAGTITIGCCCATTICGAGTICAATGGTGCACCATTCACATTGCATGATGTTCTCTCAATC 748
                                                                                                                                                                                                                                                                                361 cadciadratrinaacricaanadcacccanicaacridandacaacranacard 420
                                                                                                              TICGIATIGGICAAGACAICTAGGAAAGCAAGGGIGGAAAITIGAGAITICAGAIGACICG 688
                                                                                                                                                                 Trrarccradircadaccccaccrcardcrardradaagridaaararcagaagarard 360
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                                                                                                                                                                                                                                                                                                                                            CTTGAGGGGGTAAGGCGTAACAGCATAGGAAGAGCTGGCCGCGC 792
                                                                                                                                                                                                                                                                                                                                                                                                  CTAAAAGAAATGCGATTCTGTGGAAGAGAACAACATGACAGCAC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C6102_1
US-10-767-795-6106
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ORGANISM: Gossypium hirsutum
                                                                                                                                                                 301
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236 ATAGITIGIGAGAAAGITGAAGCCAAAGGAAGAACAACATACAATGAGGITGCAGACGAA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 cigerercakárricaccaarrcaááraaccarrrescriecrisárresécriarsárcas 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AAGAACATTAGGCGAAGAGTTTATGATGCTTTAAATGTGCTAATGGCAATGAACATAATT 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 rcaaaggaaaaaaaaaaaaaagregarregecregecraccaarrergereagaargr 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 cagaarcregagaraangaagcagaggggaragaaggggaragaaggaaggagagaggagg 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 9; 1 Pred. No. 7.3e-13;
PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR PILING DATE: 2000-09-25

PRIOR PILING DATE: 2000-09-25

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,637

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,720

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

NUMBER: PAECATION NUMBER: US/60/235,863

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NUMBER: PAECATION NUMBER: US/60/235,863

PRIOR PILING DATE: 2000-09-27

NUMBER: PAECATION NUMBER: US/60/235,863

PRIOR PILING DATE: 2000-09-27

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PRIOR PILING DATE: 2000-09-27

NUMBER: PAECATION NUMBER: US/60/235,863

PRIOR PILING DATE: 2000-09-27
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Best Local Similarity 57.8%;
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-09-954-456-1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Job time : 693 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 ATTTATTCAGAGCTG------AAGTCCATGGCACATATTGGTCAAGGGTTTGAT 343
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Pred. No. 3.6e-13;
0; Mismatches 132; Indels 12;
                                                                                               COMPUTER: IDN PC compatible
COMPUTER: IDN PC compatible
COMPUTER: IDN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION CURROWN>
PRIOR APPLICATION NUMBER: CURROWN>
FILING DATE: CURROWN>
APPLICATION NUMBER: CURROWN>
FILING DATE: CURROWN>
APPLICATION NUMBER: CURROWN>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMUNICATION INDER: 37.071
REGISTRATION NUMBER: 37.071
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
(650) 855-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: 9604478
SEQUENCE DESCRIPTION: SEQ ID NO: 1456:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
8-09-954-456-1176
'Sequence 1176, Application US/09954456
'Patent No. US20020115057A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1456:
SEQUENCE CHARACTERISTICS:
LENGTH: 2320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.1%;
Matches 200; Conservative
                                             ZIP: 94304
COMPUTER READABLE FORM:
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Length 1266;

406

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Search completed: February 6, 2005, 17:24:00
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GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

Run on:

February 4, 2005, 20:05:19; Search time 165 Seconds (without alignments) 611.785 Million cell updates/sec

US-10-088-830-2

score:

1 MAPPRGGAAAAATAALDLTG.....SILEGVRRNSIGRAGRATLH 261 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2105692 Total number of hits satisfying chosen parameters: 2105692 segs, 386760381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003ss:\*
geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

i						
Result No.	Score	Query Match	Length	DB	. OI	Description
п	1314	9.66	261	4	AAB67762	Aab67762 Amino aci
~	890.5	67.5	294	œ	ADQ36843	Adq36843 Os018989-
٣	492	37.3	344	m	AAG22851	_
4	492	37.3	385	m	AAG22850	
S	492	37.3	385	Ŋ	AAU72542	-
y	492	37.3	385	œ	AD062143	Ado62143 Transcrip
7	492	37.3	385	œ	ADO63083	m
<b>œ</b>	471.5	35.7	346	œ	ADQ36845	Adq36845 Cell prol
6	466.5	35.4	376	Ŋ	AAU72514	Arabi
10	466.5	35.4	379	æ	ADQ36855	Adq36855 Cell prol
11	461	35.0		m	AAB07975	A COI
12	437	33.1		m	AAG22852	Aag22852 Arabidops
13	428.5	32.5	292	S	AAU72529	
14	428.5	32.5	292	9	ABP96848	Abp96848 Arabidops
15	428.5	32.5	292	7	ADH59560	Adh59560 Dimerisat
16	428.5	32.5	292	œ	ADO63085	Ado63085 Transcrip
17	428.5	32.5	292	æ	AD062145	Ado62145 Transcrip
18	428.5	32.5	296	ഹ	AAU72497	Aau72497 Arabidops
19	416.5	31.6	194	~	AAY32164	Aay32164 Corn DP-2
20	412	31.2	262	Ŋ	AAU72572	Aau72572 Arabidops
21	406.5	m	251	2	AAU72559	Aau72559 Arabidops
22	399.5	m	431	8	ADN05730	Adn05730 Antipsori
23	396.5	30.1	424	4	ABG28057	Abg28057 Novel hum
24	389	~	446	N	AAY18026	Aay18026 Murine DP
25	378.5	28.7	410	~	AAR89212	Aar89212 Transcrip

	Aag74072 Human col	Adm78625 Human tra	Ado19869 Human PRO	Aar54663 Transcrip	Aaw83389 Caenorhab	Adp12553 Protein e	Abr82450 Human ARP	Adq74871 Human and	Aab67766 Fragment	Aay32161 Impatiens	Aau72563 Arabidops	Aab67767 Fragment	Aab67765 Fragment	Aab33108 Pinus rad	Aau72569 Arabidops	Aau72557 Arabidops	Aab67768 Fragment	Aab33007 Pinus rad	Abg05510 Novel hum
ABB60852	AAG74072	ADM78625	ADO19869	AAR54663	AAW83389	ADP12553	ABR82450	ADQ74871	AAB67766	AAY32161	AAU72563	AAB67767	AAB67765	AAB33108	AAU72569	AAU72557	AAB67768	AAB33007	ABG05510
4	5	8	8	0	2	2 8	2	2 8	4	8	3	6 4	1 4	9	2	2	4	ი 0	4
445	32	41	41	41	57	34	40	40	Ŋ	13	19	26	51	11	142	14	20	12	149
28.5	28.4	28.4	28.4	28.2	26.8	22.9	22.7	22.7	21.7	21.6	21.6	20.6	20.0	19.8	19.8	19.8	19.4	19.3	18.6
375.5	374.5	374.5	374.5	372.5	354	302	299.5	299.5	286	284.5	284.5	272	264	261.5	261	261	256	254.5	245
26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation. Amino acid sequence of a wheat E2F-dimerisation partner (DP) protein. (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF. Ramirez-Parra E; AAB67762 standard; protein; 261 AA. 99ES-00002127. 99ES-00002474. 25-SEP-2000; 2000WO-EP009325. (first entry) Gutierrez-Armenta C, Triticum monococcum. WO200121644-A2. 24-SEP-1999; 11-NOV-1999; 11-JUN-2001 29-MAR-2001 AAB67762; AAB67762 

WPI; 2001-257972/26.

N-PSDB; AAF80144.

New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size.

Claim 7; Fig 1; 77pp; English.

The present sequence represents a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size

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AAG22851 standard; protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0121825P.
990S-0123180P.
990S-0125784B.
990S-0126284P.
990S-0126785P.
990S-0126785P.
990S-0128734P.
990S-0128734P.
990S-0130845P.
990S-0130849P.
990S-0130849P.
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99US-0132486P.
99US-0132487P.
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99US-0134256P.
99US-0134218P.
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99US-0132484P
                             63.1%;
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                       Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                   Query Match
Best Local Similarity
Sequence 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1999;
01-APR-1999;
06-APR-1999;
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23-APR-1999;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1999;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                   17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related polypeptide. The present sequence is published separately from the main body of the
                                                   ö
                                                                                                                                                                                                      240
                                                                                                           RITGMGLREYSKIVCEKVEAKGRTTYNEVADBIYSELKSMAHIGGGFDEKNIRRRVYDAF 120
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                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response.
                                                                                                                                                                                           ONIKLRNOTLESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDD
                                                                                 1 MAPPRGGAAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVDPDXDRKKEKAAAP
                                                                                                                                                   NVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDL
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for
                                                  ö
                               Length 261;
                                                  Indels
                              99.6%; Score 1314; DB 4; 99.6%; Pred. No. 5.6e-115;
                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 28; SEQ ID NO 2; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                  LSILEGVRRNSIGRAGRATLH 261
                                                                                                                                                                                                                                             ADQ36843 standard; protein; 294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             producing enhanced food crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2002; 2002US-0436565P.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                         Best Local Similarity 99.6
Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Os018989-4003 protein.
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             Sequence 261 AA;
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                                                                                                                                                                                                                                                                                                                     144 YRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVNGIRLP 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                      61 KKSVSLRSGGGGNAAEREEGGA---NRNGKKEKTGAQRITGWGLREFSKIVSKKVEAKGR
                                                                                                                                                                                                                                                                                                                                            35 -----AGGNAVORK--GAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGR
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     204 FVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNSIGRAG 256
                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 294;
                                         Indels
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    DB 8;
                                                                                 1 MAPPRGGAAAAATAALDLTGVHILEASSVPPLPE-----
  67.5%; Score 890.5; DB 8 63.1%; Pred. No. 4.7e-75;
                                         31; Mismatches
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RR 27-UUL-1999; 99US-01453918P

RR 28-UUL-1999; 99US-01453918P

RR 28-UUL-1999; 99US-01453918P

RR 02-AUG-1999; 99US-01453918P

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RR 02-AUG-1999; 99US-0145389P

RR 03-AUG-1999; 99US-0143918P

RR 03-AUG-1999; 99US-0147302P

RR 03-AUG-1999; 99US-0147302P

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RR 13-AUG-1999; 99US-0149318P

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RR 11-AUG-1999; 99US-0155029P

RR 11-AUG-1999; 99US-01550

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9905-0139455P

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07-JUN-1999;
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14-JUN-1999;
16-JUN-1999;
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17-JUN-1999;
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22-JUL-1999;
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  LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS 210
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                                                                                                                                                                                  Gaps
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                                                                                                                                                     37.3%; Score 492; DB 3; Length 344; 47.7%; Pred. No. 1.8e-37; ive 40; Mismatches 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG22850 standard; protein; 385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0121825P.
99US-0123180P.
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              99US-0161405P.
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99US-0161932P.
99US-0161993P.
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  99US-0161404P
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                                                                                                                                                                       Best Local Similarity 47.7 Matches 104; Conservative
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                                                                                                                                                                     Similarity
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05-MAR-1999,
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04-MAY-1999;
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Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen.
                                                                                                                                                                                                                                                                                                                          New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
                                                                                                                                                                                                                                                                                                                                                                                  37 GNAVORKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRITYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                               152 LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
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larity 47.7%; Pred. No. 2.2e-37;
Conservative 40; Mismatches 68; Indels
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               9905-0160815P-
9905-0160810P-
9905-0160981P-
9905-0161404P-
9905-0161405P-
9905-016155P-
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9905-016195P-
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N-PSDB; AAS96332.
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Best Local Similarity
Matches 104; Conserv
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   21-0CT-1999;
22-0CT-1999;
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AAU72542
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99US-0147192P.
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31-Aug-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
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22-JUL-1999;
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23-JUL-1999;
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27-JUL-1999;
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27-JUL-1999;
28-JUL-1999;
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10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
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09-AUG-1999;
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17-AUG-1999;
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Arabidopsis thaliana.

The invention relates to a novel cell cycle protein (CCP) and the polympical conditates the activity of the polympication and which binds to the which modulates the activity of the polympical and which binds to the polympication and the activity of the polympication and the presence of CCP in a sample. A CCP antibody is useful for detecting the presence of CCP in a sample. A CCP antibody is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thallana, rice, wheat, maize, tomato, alfalfa, oilseed trape, soybean, sumflower and canola. CCC maize, tomato, alfalfa, oilseed trape, soybean, sumflower and canola. CCC maize, tomato, alfalfa, oilseed trape, soybean, sumflower and canola. CCC conclete cated and polympication molecules are useful as modulating agents in plants. CCP is useful to treat abscrant activity. Compounds that bind to or modulate the activity of CCP protein or production of CCP protein forms which have decreased or abscrant activity. Compounds that bind to or modulate the activity of CCP polympicate are useful for modifying cell fate, plant development, plothemistry and/or physiology, the length of the CC polympication or enhancement of cell division, DNA replication, seed set, plant morphology, blothemistry and/or physiology, the length of the CC stimulation or enhancement of cell division, DNA replication, seed set, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, about an droot continuate or resistance to stress cop, the polymclectide and the anti-CCP antibody are useful in agriculture to modulate the complete cop environmental conditions, including abjotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attendate cop pathogen attack, to modulate e.g. enhance cop pathogen attack, to modulate e.g. enhance cop is useful for expressing CCP percarge organs of plants quality traits, plant reproduction and seed development, endocadulatein is useful to screen for naturally cocur 

Sequence 385 AA;

152 LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS 210 |: | |: | |: | | | | ||: ||: || || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 97 LKSMAHIG-----OGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151 96 37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNBVADEIYSE 9 37.3%; Score 492; DB 5; Length 385; 47.7%; Pred. No. 2.2e-37; ive 40; Mismatches 68; Indels 211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248 254 PHATVEVEISEDMQLVHFDFNSTPFELHDDNFVLKTMK 291 Matches 104; Conservative Best Local Similarity Query Match 셤 ð 셤 셤 à ò

Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low mitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development. Transcription factor G2981, SEQ ID 610. ADO62143 standard; protein; 385 AA. (first entry) 15-JUL-2004. ADO62143; ADO62143 ID ADO6 RESULT 6 

Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS, (MEND-) MENDEL BIOTECHNOLOGY INC. 17-DEC-2002; 2002US-0434166P. 24-APR-2003; 2003US-0465809P. 18-SEP-2003; 2003WO-US030292. .8-SEP-2002; 2002US-0411837P. WPI; 2004-330163/30. WO2004031349-A2 15-APR-2004 

Reuber TL;

Adam LJ, R Sherman BK;

New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant. N-PSDB; ADO62142

Claim 14; SEQ ID NO 610; 510pp; English

The present invention relates to novel plant transcription factor

proteins (1) and nucleotide sequences (II) (ADO61534-ADO6378). The

sequences can be used to produce transgenic plants, which overexpress

(II), where the transgenic plant has an allered trait as compared to a

non-transgenic plant or wild-type plant. The transgenic plant comprises

an altered trait selected from increased tolerance to callot, stress,
increased germination in cold, increased tolerance to cold,
increased germination in heat, increased tolerance to cold,
increased germination in heat, increased tolerance to disease, including

continuation in heat, increased tolerance to disease, including

thomsphate conditions, increased tolerance to disease, including

content of the planticularly Eryaphe, Rusarium and Botryfis,
increased sensitivity to ACC, altered sugar sensing, increased tolerance

contenessed sensitivity to ACC, altered sugar sensing, increased tolerance

contenessed sensitivity to ACC, altered sugar sensing, increased tolerance

contenessed sensitivity to ACC, altered sugar sensing, increased tolerance

contenessed sensitivity to ACC, altered sugar sensing, increased tolerance

contered carbon/nitrogen sensing, early flowering, attered

contered trichome structure, loss of flower determinacy, reduced

contered trichome structure, altered branning pattern,
altered stem morphology, altered ascular tissue structure, reduced

apical dominance, altered trichome density, altered trichome development,
altered call proliferation, altered coll expansion, altered shade

condensed sensescence, abnormal embry development, altered bange,
altered call proliferation, altered call expansion, altered shade

contered sensescence, abnormal embry development, altered phase change,
altered sensescence, abnormal embry development, altered proper and mass, light

cond increased biomass, large seedlings, darfed plants, altered seed

cond increased biomass, large seedlings, altered seed solarge,
altered seed coloration, altered seed singhes, alter seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

37.3%; Score 492; DB 8; 47.7%; Pred. No. 2.2e-37; tive 40; Mismatches 68 Best Local Similarity 47.78 Matches 104; Conservative Sequence 385 AA; Query Match

37 GNAVORKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRITYNEVADEIYSE

Gaps . 9

Length 385; 68; Indels à

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ADQ36845 standard; protein; 346
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungal disease and particularly Erysiphe, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern,
                                                                 210
           97 LKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151
                           Plant; transcription factor; transgenic plant; abiotic stress tolerance; sembits estress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phobbate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (11) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to ablotic stress, increased tolerance to condition in cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold increased demandation in heat, increased tolerance to learn to tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to low phosphate conditions, increased tolerance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                LEEVRKELVNKI RNKKALLQEI EKQFDDLQNI KLRNQTLESSAENVN-GIRLPFVLVKTS
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Sherman BK;
                                                                                                                    211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                    254 PHATVEVEISEDMOLVHFDFNSTPFELHDDNFVLKTMK 291
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Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                  Transcription factor G2981, SEQ ID 1550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1550; 510pp; English
                                                                                                                                                                                                                   ADO63083 standard; protein; 385 AA
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V, Dubell Al
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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altered stem morphology, altered vascular tissue structure, reduced
apical dominance, altered trichome density, altered trichome development,
altered trichome structure, altered root development, altered shade
avoidance, altered seed development, altered seed ripening, altered seed
avoidance, altered seed structure, altered cell differentiation,
content, lethality when overexpressed, altered necrosis pattered phase change,
altered senescence, abnormal embryo development, altered programmed cell
catch, lethality when overexpressed, altered necrosis patterns, increased
plant size, increased blomass, large seedlings, dwarfed plants, dark
green leaves, change in leaf shape, increased leaf size and mass, light
cgreen leaves, change in leaf shape, increased leaf size and mass, light
cgreen or gray leaves, glossy leaves, altered seed shape, large
altered seed coloration, altered seed size, altered seed shape, large
content, altered seed protein content, altered seed seed oil
content, altered seed protein content, altered seedprenyl content,
altered leaf prenyl lipid content, increased anthocyanin levels, and
decreased anthocyanin levels. Note: The sequence data for this patent did
cnot form part of the printed specification, but was obtained in
celectronic format directly from WIPO at
cleb wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.3%; Score 492; DB 8; Length 385; 47.7%; Pred. No. 2.2e-37; ive 40; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
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The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related polypeptide. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKKEKAAAPRIT----GWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIGQG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 PDPDNPNTPQFDEKNIRRRVYDALNVLMAMDIISKDKKEIQWKGLPR---TSMSDVEELK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTSRK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
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polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Magyar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.7%; Score 471.5; DB 8 39.6%; Pred. No. 1.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches
                                                                                                                            Claim 28; SEQ ID NO 4; 408pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU72514 standard; protein; 376 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 113; Conservative
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N-PSDB; AAS96304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200185946-A2
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The invention relates to a novel cell cycle protein (CCF) and the polymucleotides encoding them. CCF is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for identifying a compound of CCF in a sample. A CCP modulator is useful for modulating the presence of CCP in a sample. A CCP modulator is useful for modulating the presence of CCP in a sample. A CCP modulator is useful for wheat, sumflower and canola. CCP maiole, all properties are useful as modulating agents in regulating call cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polypeptide are useful as herbicides or plant growth regulators. The polypeptide are useful as herbicides or plant growth regulators. The polypeptide are useful for modifying cell fate, plant development, stimulation or enhancement of cell division, DNA replication, seed set, S G2 and/or M phase of the cell cycle of a plant, initiation promotion, stimulation and/or development, under function, dwarfism in plants, initiation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, underly function, dwarfism in plants, continitiation heat, arought, salt stress, or bictic stress such as cold, nutrient protein levels or activity of a protein involved in the cell cycle due to protein levels or activity of a protein involved in the cell cycle due to pathogen attack, to modulate e.g. enhance crop yields, and attenuate plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for attually companies. CCP substrates. The polymorphic is useful for avpressing CCP modulate CCP activity. The present sequence represents a CCP protein of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                              invention relates to a novel cell cycle protein (CCP) and the mucleotides encoding them. CCP is useful for identifying a compound
New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 LKNERLSLRNRIEKKTAYSOELEEQ-----RNEHLYSSGNAPSGGVALPFILVOTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 PHATVEVEISEDMOLVHFDFNSTPFELHDDNFVLKTMK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.4%; Score 466.5; DB 5
46.3%; Pred. No. 5.2e-35;
ive 38; Mismatches 64
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                                                                                                        Claim 34; Page 227-228; 316pp; English
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Matches 101; Conservative
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DNA replication; DRTF; differentiation-regulated transcription factor 1; transgenic plant; transformation efficiency.
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ID AAG22852 standard; protein; 277
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                                                                                                                                                                                                                                                    N-PSDB; AAA59702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 299 AA;
                                                                    Misc-difference
                                                                                                     WO200047614-A1
                                                                                                                                                                     12-FEB-1999;
                                                                                                                                                                                                                                                                                                              the plant.
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                                                                                                                                                                                                                                                                                            The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related polypeptide. The present sequence is published separately from the main body of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 KGLPR---TSINDIEDL@TELVGLKSRIEKKNTYL@EL@DGFVGMOKLIORNEOLYGSG- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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 proliferation related polypeptide; cell proliferation; senescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 PPSGGAOSASTSG-----GSAGSPSSRSEOHVPAAAGMAAGAAASTPISENTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP polypeptide; transcription factor; gene transcription; cell cycle;
                                                                                                                                                                                                               New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NV -- NGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                                                                                        35.4%; Score 466.5; DB 8; Length 379; 37.8%; Pred. No. 5.3e-35; Live 43; Mismatches 77; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A corn transcription factor designated DP.
                                                                                                                                                                                                                                                                       Claim 28; SEQ ID NO 14; 408pp; English.
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           differentiation; stress response
                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                producing enhanced food crops
                                                                                                                       26-DEC-2002; 2002US-0436565P.
                                                                                                   2003WO-US041200
                                                                                                                                                                                                                                                                                                                                                                              specification as EPO data.
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                                                                                                                                                                                         WPI; 2004-534388/51.
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es 111; Conserv
                                                      WO2004061122-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 379 AA;
                                 Oryza sativa
                                                                                                  23-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-2000
                                                                                                                                                                     Cooper B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic plants comprising an expression cassette consisting of a DP nucleic acid, when expressed, the nucleic acid increases the efficiency of plant cell transformation by increasing the number of dividing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 QNLIQRNEQSYGSGNTPSGGVALPFILVQTRPHATVEVEISEDMQLVHFDFNSTPFELHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDLTGVHILEASSVPPLPEAGGNAVQRKG--AVDPDKDRKKEKAAAPRITGWGLREYSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LDING------GLROAPSSQAPTSKKKRRGTRAVGPDKGNR-------GLROFSMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 VCEKVEAKGRITYNEVADEIYSELKSMAH-----IGQGFDEKNIRRVYDAFNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 IALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELV---NKIRNKKALLQEIEKQFDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNIKLRN-QTLESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a corn DP (not defined) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
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                                                                  /note= "any amino acid encoded by NNN'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gregory CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%; Score 461; DB 3; 40.7%; Pred. No. 1.2e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 71-72; 76pp; English.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC
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9905-0139463P-
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9905-0139617P-
9905-013969P-
9905-0140353P-
9905-014033P-
9905-014033P-
9905-014039P-
9905-014039P-
9905-01423P-
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9905-01423P-
9905-01433P-
9905-014433P-
9905-014508P-
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9905-0149175P-
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23-AUG-1999;
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02-AUG-1999
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 25937.
                                                                                                                                                                                                                                                        9905-01231800

9905-0123548P

9905-0125788P

9905-0126785P

9905-0128714P

9905-0128714P

9905-0130449P

9905-0130449P

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9905-0131449P

9905-0132448P

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9905-013424P

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9905-0139452P

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9905-0139454P

9905-0139458P
                                                                                                                                                                                                                     2000EP-00301439
                                    (first entry)
                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                            25-PEB-1999, 05-MAR-1999, 23-MAR-1999, 22-MAR-1999, 22-MAR-1999, 22-MAR-1999, 06-APR-1999, 06-APR-1999, 23-APR-1999, 23-APR-1999, 06-MAY-1999, 06-MAY-1999, 14-MAY-1999, 14-MAY-1999, 14-MAY-1999, 14-MAY-1999, 14-MAY-1999, 14-MAY-1999, 11-MAY-1999, 11-MA
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18-JUN-1999;
18-JUN-1999;
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                                    17-OCT-2000
                                                                                                                                                                   EP1033405-A2
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          AAG22852;
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99US-0151080P.
99US-0151303P.
99US-0151438P.
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99US-0161993P.
99US-0162142P.
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                                           99US-0151930P.
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                  99US-0151066P
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                                                                     99US-0154018P
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14-0CT-1999;
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VCEKVEAKGRTTYNEVADEIYSELKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRV 128
                                                                                        IAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQ 188
                                                                                                  Gaps
                       9
Query Match 33.1%; Score 437; DB 3; Length 277; Best Local Similarity 50.3%; Pred. No. 2e-32; Matches 91; Conservative 32; Mismatches 52; Indels
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invention

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The invention relates to a novel cell cycle protein (CCP) and the polymorlectides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for adulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CC cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, candle card and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or personal activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or polymeptide are useful as herbicides or plant growth regulators. The polymorlectide is useful for modifying cell fate, plant development, of plant morphology, biochemistry and/or physiology, the length of the G1, S2 and/or M phase of the cell cycle of a plant, initiation, promotion, grimulation or enhancement of cell division, DNA replication, seed set. Strimulation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, module function, dwarfing min plants.

Scaladon, heat, drevelopment, module function, dwarfing min plants, send the anti-CCP antibody are useful in agriculture to modulate the continuous or resistance to stress. CCP, the polymorlectide conditions, including ablocic stress such as cold, mutrient deprivation, heat, drought, salt stress, or biotic stress such as cold and the anti-CCP antibodies. CCP pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant quality traits, plant reproduction and seed development, and ground in stress cold in the cell cycle due to generate antibodies. CCP protein is useful for expressing CCP protein, co 
                                                                                                                                                                                                                         Cell cycle protein; CCP; cell cycle regulation; herbicide;
plant growth regulator; plant development; abiotic stress; biotic stress;
nutrient deprivation; pathogen attack; crop yield; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Veylder L, Acosta JAT, Magyar Z;
                                                                                                                                                                                 Arabidopsis cell cycle protein CCP16.
                                            AAU72529 standard; protein; 292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 34; Fig 16; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-2001; 2001WO-IB001307.
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                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inze D, Boudolf V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-062249/08.
N-PSDB; AAS96319.
                                                                                                                                                                                                                                                                                                                                                                   WO200185946-A2.
                                                                                                                                    26-FEB-2002
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                                                                                       AAU72529;
RESULT 13
AAU72529
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Gaps

7;

IndelB

69

49; Mismatches

Length 292;

32.5%; Score 428.5; DB 6; 41.3%; Pred. No. 1.4e-31;

41.38;

Query Match 32.5 Best Local Similarity 41.3 Matches 88; Conservative

Sequence 292 AA;

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66 86 100 MAHIGQ-----GPDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLE 153

40 VQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS

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154 EVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAEN-VNGIRLPFVLVKTSRK 212

Sequence 292 AA;

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100 MAHIGQ-----GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLE 153
                                                                                                   154 BVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAEN-VNGIRLPFVLVKTSRK 212
                                                                                                              66
                                                 86
                                          40 VQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS
                Gaps
                7;
Length 292;
                                                                                                                                                                                                                                                              Arabidopsis thaliana, modulation, endoreduplication, plant, transgenic plant, cell cycle, E2F; DP.
       ; Pred. No. 1.4e-31;
49; Mismatches 69; Indels
32.5%; Score 428.5; DB 5;
                                                                                                                                    ARVEIEISDDSKFAHFEFNGAPFTLHDDLSILE 245
                                                                                                                                             | ||||||:| : | :|| ||::||| ||: 339
                                                                                                                                                                                                                                              Arabidopsis thaliana DP protein SEQ ID NO:4.
                                                                                                                                                                                              ABP96848 standard; protein; 292 AA
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                                                                                                                                                                                                                                                                                                                                                           24-AUG-2001; 2001US-00938342
       41.3%;
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                88; Conservative
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                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
       Best Local Similarity
Matches 88; Conserv
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Query Match
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The present invention relates to increasing the cell number of specific cell types, specific tissues or specific organs in a plant comprises modulating the expression and/or the activity in the specific cell types, specific tissues or specific organs of the plant E2F transcription factor. The E2F transcription factor or its homologue, derivative or fragment, is useful for prolonging the period of cell division in certain cells and tissues, for increasing the size of cotyledons, for enhancing cell proliferation after seed germination, for enhancing stress resistance of seedlings, for obtaining seedlings with enhanced vigor, for obtaining plants that have increased growth or number of organs, for obtaining plants having more cells in a particular tissue, for obtaining plants having an increased size of organs or having increased yield, for stimulating differentiated cells to re-enter the cell cycle, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying cell number, architecture and yield of plants comprises modulating the expression and/or the activity of members of the plant E2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mironov V, Broekaert W;
                                                                                                                                                                              E2F transcription factor; Gene therapy; stress resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; SEQ ID NO 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inze D,
                                     Ż
                                     ADH59560 standard; protein; 292
                                                                                                                                                                                                                                                                                                                                                 12-SEP-2002; 2002WO-EP010236.
                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2001; 2001EP-00870198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulating the expression an transcription factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Veylder L,
                                                                                                          (first entry)
                                                                                                                                                                                                   differentiation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frankard V;
                                                                                                                                                                                                                                                                                                                                                                                                                        (CROP-) CROPDESIGN NV.
                                                                                                                                              Dimerisation partner.
                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-371815/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADH59559
                                                                                                                                                                                                                                                                         WO2003025185-A1.
                                                                                                            25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beeckman T,
                                                                                                                                                                                                                                                                                                             27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillen W,
                                                                        ADH59560;
RESULT 15
                    ADH59560
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The present invention describes a method for modulating endoreduplication in a plant, or a part of the plant. The method comprises modifying the expression or activity of an E2F and DP gene or polypepitide. Also described: (1) a transgenic plant cell overexpressing an E2F or E2Fa gene, or an E2F and DP gene or an E2Fa and DP gene, where the E2F or E2Fa gene, or an E2F and DP gene is under the control of a tissue or cell-type specific promoter; (2) a transgenic plant, or a part of the plant, comprising the cells described above; (3) a progeny of the plant described above; and (4) a plant material obtained from the plant described above; The method is useful in modulating plant cell cycle proteins by modifying the expression or activity of an E2F and DP gene or polypeptide. The present sequence represents Arabidopsis thaliana DP, which is used in the exemplification of the present invention

Modulating endoreduplication in a plant, or a part of the plant, comprises modifying the expression or activity of an B2Fa and DPa gene or

Disclosure, Page 26-27; 34pp; English.

polypeptide.

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Segers

Mironov V,

De Veylder L, Inze D,

WPI; 2003-300735/29.

N-PSDB; ACC45100

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overriding the cell differentiation signals, or for altering cell shape. The present sequence represents the dimerisation partner.
ន្តដូល
```

Sequence 292 AA;

Query Match 32.5%; Score 428.5; DB 7; Length 292; Best Local Similarity 41.3%; Pred. No. 1.4e-31; Matches 88; Conservative 49; Mismatches 69; Indels 7; Gaps දු දු

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Search completed: February 4, 2005, 20:30:04 Job time: 168 secs

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us-10-088-830-2.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

February 4, 2005, 20:21:34; Search time 39 Seconds (without alignments) 643.912 Million cell updates/sec Run on:

US-10-088-830-2 1319 1 MAPPRGGAAAAATAALDLTG......SILEGVRNSIGRAGRATLH 261 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\* Database :

piri: piri: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..."

STIMMARIES

	Description	transcription fact	DP-2 transcription	hypothetical prote	transcription fact				hypothetical prote	-	hypothetical prote	Ψ	$\omega$		œ	translation initia	hypothetical prote		transcription fact		transcription fact	surface membrane p	E2F-1 transcriptio	glucuronosyltransf	hypothetical prote	hypothetical prote		ical	e nucl	pole body
SUMMARIES	0	T48364	T48268	T12511	B48585	\$30049	B55745	A48585	T25207	24929	T31602	B90395	T27066	T27067	B70356	B87254	T26346	T38077	A56209	T44307	A54595	B54497	S58345	T09595	C71622	T50346	T26006	472	1023	26710
	DB ID	Ļ					2 B													_									∺	S
	Length	413	288	416	410	429	377	410	598	437	470	864	717	717	. 1156	1037	342	1957	430	496	437	337	403	972	1979	491	736	821		944
d	Query Match	34.6	32.5	30.1	28.7	28.7	28.5	28.4	26.8	9.7	9.1	8.8	8.5	8.5	8.5	8.5	8.2	8.2	8.1	8.1	8.0	7.9	7.8	7.7	٠	7.7	•	7.7	7.7	7.6
	Score	456	428.5	396.5	378.5	378.5	375.5	374.5	354	128.5	120.5	116.5	112.5	112.5	112.5	112	108.5	108.5	107	107	105	104.5	102.5	101.5	101.5	101	101	101	101	100
	Result No.	П	7	m	4	Ŋ	9	7	89	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

243 ILEGVR 248 :|: :: 314 VLKTMK 319

g ò ď RESULT 2
148268
DP-2 transcription factor-like - Arabidopsis thaliana
NP-3 transcription factor-like - Arabidopsis thaliana
CF Species: Arabidopsis thaliana (mouse-ear cress)
CF Species: Arabidopsis thaliana (mouse-ear cress)
CF Species: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

myosin heavy chain	hypothetical prote	conserved hypothet	chromosome segrega	hypothetical profe	probable ATP /GTP	ATPase involved in	hypothetical prote	bps2 protein - Des	conserved hypothet	embryonic muscle m	protein F10C1.2a [	E2F-5 - mouse	transcription fact	1-phosphatidylinos	hypothetical prote
\$18199	D84829	A70387	154383	D71453	A81385	G97236	T05634	S22195	F75103	A59236	D88163	148338	JC5833	A28821	869023
0	2	N	~	7	~	N	N	~	~	~	~	~	~	~	7
1039	416	978	1233	279	728	1163	1496	582	880	1927	558	335	346	1216	410
7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.3
100	99.5	99.5	66	98.5	98.5	98.5	98.5	86	98	98	97.5	97	97	97	96.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT T48364 transcr N;Alter C;Speci	RESULT 1 148364 Laranscription factor-like protein - Arabidopsis thaliana N;Alternate names: protein F12E4.160 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20.Apr-2000 #sequence_revision 20.Apr-2000 #text_change 09-Jul-2004
R; Bevan submitt	R. Reven, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000
A;Reter A;Acces A;Statu	A;Keterence number: 224492 A;Accession: T48364 A;Status: preliminary
A; Molec A; Regid	A;Molecule type: DNA A;Residues: 1-413 <bev></bev>
A; Cross	A:Cross-references: UNIPROT:Q9LZE7; EMBL:AL162751 A:Experimental source: cultivar Columbia: BAC clone F1284
C, Genetics:	ics:
A;Map p A;Intro A;Note:	Aintrons: 84/2; 128/1; 142/3; 163/3; 212/3; 249/1; 279/3; 303/2 Aintrons: 84/2; 128/1; 142/3; 163/3; 212/3; 249/1; 279/3; 303/2 A;Note: F12E4:160
Query Best	13;
Match	Matches 103; Conservative 41; Mismatches 68; Indels 34; Gaps 4;
ò	37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVE 79
ą	
δ	80 AKGRITYNEVADEIYSELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
qq	:
ò	135 EIRWAGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNI 183
q	194 EIGWRGLPRTSLSDIBELKNERLSLRNRIEKKTAYSQELEEQVMNIIDTLGLSASCLQNL 253
ò	184 KLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDSKPAHFEFNGAPFTLHDDLS 242

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A;Residues: 'M',33-49 <ZHA2>
A;Cross-references: EMBL:U35117; NID:g1008545; PIDN:AAC50642.1; PID:g1008546
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A,Residues: 388-410 <GIZ>
A,Cross-references: EMBL:X72310
Superfamily: transcription factor DP
C,Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor DRTF1 chain 1 - mouse
                                                                                                                                                                                                       A;Cross-references: GDB:638814
A;Map position: 3q23-3q23
A;Note: DKFZp434G222.1
C;Superfamily: transcription factor DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PRGGAAAAATAALDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 33.99
Matches 101, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                   A; Gene: GDB: TFDP2; DP2
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                                                                                                                     C, Genetics:
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NyAlternate names: E2F dimerization partner 2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: J3-Jul-1999 #sequence revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12511, A57381; I37297; I39180
R;Amsorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: I217527
A;Residues: preliminary
A;Molecule type: man
A;Residues: Left c.ANS
A;Cross-references: UNIPROT: 09UG28; EMBL:AL080206
A;Experimental source: adult testis; clone DKFZp434G222
A;Experimental source: adult testis; clone DKFZp434G222
A;Experimental source: adult testis; clone DKFZp434G222
A;Festerence number: A57381; MUID:95257935; PMID:7739337
A;Accession: A57381
A;Status: preliminary
A;Accession: A57381
A;Status: preliminary
A;Accession: A57381
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A;Accession: A57381
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A;Accession: A57381
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C;Accession: T48268
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
A;Reference number: 224490
A;Reference number: April 2000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 kBV>
A;Residues: 1-288 kBV>
A;Residues: 1-288 cBV>
A;Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 VRRKLIVDDDSEIGSEKKGGSRISGGGLRQFSVMVCQKLEAKKITTYKEVADEIISDFAI 82
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A;Molecule type: mRNA
A;Residues: 'M',33-143,'Q',144-416 <ZHA1>
A;Cross-references: EMBL:U18422; NID:g604478; PIDN:AAB60378.1; PID:g604479
A;Accession: I39180
A;Accession: I39180
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 VORKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
32.5%; Score 428.5; DB 2; Length
Best Local Similarity 41.3%; Pred. No. 4.3e-21;
Matches 88; Conservative 49; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introns: 36/2; 57/1; 71/3; 95/3; 142/3; 165/3; 198/3; 222/2
A;Note: T22P11.60
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 1.1-Nov-1994 #sequence revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: B46585, 538372; 538371
R;Helin, K.; Wu, C.L.; Fattaey, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow, E. Genes Dev. 7, 1885-1861, 1993
A;Title: Heterodimerization of the transcription factors E2F-1 and DP-1 leads to cooperat. A;Reference number: A48585; MUID:94010284; PMID:8405995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Status: preliminary, nucleic acid sequence not shown; not compared with conceptual trarral A, Status: preliminary, nucleic acid sequence not shown; not compared with conceptual trarral A, Status: preliminary and vHEL>
A, Cross-references: UNIPROT:Q08639
A, Status: preliminary
A, Molecule type: mRNA
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-410 < GIR>
A, Residues: 1-410 < GIR>
A, Residues: 1-410 < GIR>
A, Residues: 1-410 < GIR>
A, Residues: 1-410 < GIR>
A, Reference on maper: MRNA
A, Residues: 1-410 < GIR>
A, Reference on maper: S18371; MUID:94019777; PMID:8413592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 DEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYE 147
                                                                                                                                                                                                                                                                                                                                                                                                                148 KIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLP 203
                                                                                                                                                                            12 PSPGTESAGTFILDLSATSRTIISTPQRLTSSGSVLIGSPYTPAPAMVTQTHIAEATGWV 71
                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 FVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRRNSIGRAGRATL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 FIIINTSRKTVIDCSISSD-KFEYLFNFDNT-FEIHDDIEVLKRMGMSFGLESGKCSL 301
                                                                                                                                                                                                                                                        31 PLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVA
                                                              Gaps
   Length 416;
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                                                              Indels
   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
28.7%; Score 378.5; DB 2;
Best Local Similarity 42.4%; Pred. No. 1.2e-17;
Matches 87; Conservative 41; Mismatches 60;
30.1%; Score 396.5; DB 2; 33.9%; Pred. No. 8.4e-19; tive 52; Mismatches 96;
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115

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CyAccession: A48585
R.Helin, K.; Wu, C.L.; Fattaey, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow, E. Genes Dev. 7, 1850-1861, 1993
A,Title: Heterodimerization of the transcription factors E2F-1 and DP-1 leads to cooperat A,Reference number: A48585, WUID:94010284; PMID:8405995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-410 <HEL>
A; Residues: 1-410 <HEL>
A; Cross-references: UNIPROT: Q14186; GB:L23959; NID:g414316; PIDN:AAA58440.1; PID:g414317
C; Superfamily: transcription factor DP
C; Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                       50 KDRKKEKAAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 GFDEKVIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRN 165
                                                                                                                                                                                                                                                                                                                                                              81 KGRTTYNEVADEIYS-ELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 GLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESS----AE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T23G7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Homo sapiens (man)
C,Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 KQSQLQELILQQIAPKNLVQRNRHAEQQASRPPPPNSVIHLPFIIVNTSKKTVIDCSISN
                                                                                                                                                                                                                                                                                             105 RNRKGEK-----NGKGLRHFSMKVCEKVQRKGTTSYNEVADELVAEFSAADNHILPNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 VHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                 A,Cross-references: UNIPROT:Q24318; GB:X79708; NID:g516866; PID:g516867
C;Genetics:
A,Gene: Flybase:Dp
A,Gross-references: Flybase:FBgn0011763
C;Superfamily: transcription factor DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 NAS-IQLPFIIVNTHKSTKINCSVTNDKSEYIFKFD-KTFEMHDDIEVLK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 NVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILB 245
                                                                                                                                                                    Length 377;
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                                                                                                                                                                 / Match 28.5%; Score 375.5; DB 2; Local Similarity 39.1%; Pred. No. 1.8e-17; nes 90; Conservative 49; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary, nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.4%; Score 374.5; DB 2;
42.0%; Pred. No. 2.3e-17;
tive 42; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 DSKFAH-FEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor DP-1 - human
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Best Local Similarity
Matches 86; Conserva
A; Residues: 1-377 < DYN>
                                                                                                                                                                    Query Match
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Matches
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NyAlternate names: transcription factor DP-1

Syspeciaes: Mus musculus (house mouse)

C;Speciaes: Mus musculus (house mouse)

C;Speciaes: 30-68p-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999

C;Accession: S30049; S34572

C;Accession: S30049; S34572

Sysfairling, R.; Partridge, J.F.; Bandara, L.R.; Burden, N.; Totty, N.F.; Hsuan, J.J.; la Nature 362, 83-87, 1993

A;Title: A new component of the transcription factor DRTF1/E2F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor DP - fruit fly (Drosophila melanogaster)
(Species: Drosophila melanogaster
Cjate: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004
CjAccession: B55745
R;Dynlacht, B.D.; Brook, A.; Dembski, M.; Yenush, L.; Dyson, N.
Proc. Natl. Acad. Sci. US.A. 91, 6359-6363, 1994
A;Title: DNA-binding and trans-activation properties of Drosophila E2F and DP proteins.
A;Reference number: A55745; MUID:94294381; PMID:8022787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <GIR2>
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                           106 GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRN 165
                                                                                                                      KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEİSD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GFDEKUIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYBKIKKLEEVRKELVNKIRN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
R,Molecule type: protein
C,Superfamily: transcription factor DP
C,Keywords: DNA binding; transcription factor
F,84-204/Domain: DNA binding #status predicted <DNA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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A;Scatus: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.7%; Score 378.5; DB 2; 42.4%; Pred. No. 1.3e-17; ive 41; Mismatches 60;
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A,Accession: S34572
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Best Local Similarity 42.4%
Local Similarity 42.4%
Conservative
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A, Molecule type: mRNA
A, Residues: 1-429 <GIR1>
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9.1%; Score 120.5; DB 2; Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 24.3% Matches 64; Conservative
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R;Barlow, K.
Bubmitted to the EMBL Data Library, December 1995
A;Reference number: 21995
A;Accession: T25207
A;Accession: T25207
A;Accession: Freliminary; translated from GB/EMBL/DDBJ
A;Acture: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-598 <WIL>
A;Residues: 1-598 <WIL>
A;Residues: 1-598 <WIL>
A;Cross-references: UNIPROT:Q22703; EMBL:Z68319; PIDN:CAA92699.1; GSPDB:GN00020; CESP:TZ
C;Genetics:
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A,Molecule type: mRNA
A,Residues: 1-312, 'S', 314-321,'N', 323-328,'T',330-437 <HEL>
A,Cross-references: GB:M96577; NID:g181917; PIDN:AAA35782.1; PID:g181918
A,Experimental Bource: Nalm 6 pre-B leukhamia cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:110015, NCBIP:110016)
R;Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; DeCaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                       A, Introns: 3/3; 115/3; 204/2; 227/2; 260/1; 298/1; 363/1; 424/3; 478/3; 565/1
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Best Local Similarity 41.3*
Matches 78; Conservative
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IHDDFEILK 259
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A;Map position: 2
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A; Molecule type: mRNA
A; Residues: 1-312, 'S',314-321,'N',323-328,'T',330-437 <KAE>
A; Residues: 1-312,'S',314-321,'N',323-328,'T',330-437 <KAE>
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A; Reference number: 154091; MUID:g5047311; PMID:7958836
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A;ross-references: GB:134661; OMIM:189971
A;Map position: 20q11-20q1
A;Introns: 87/3 118/1 191/2 242/2 280/3 356/1
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F;718-190/Domain: DNA binding #status predicted <DNA>
F;118-190/Domain: DNA binding #status predicted <DNA>
A;Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F-A;Reference number: A42997; MUID:92346721; PMID:1638635
A;Accession: A42997
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C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T31602
R.Wallis, J.
R.Wallis, J.
R.Wallis, J.
R.Kaference number: Z21046
A.Accession: T31602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AKKSKNHIQWLG-SHTTVGVGGRLEGLTQDL-----RQLQESEQQLDHLMNICTTQL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: I54091
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-88,'R','T','122-123,'TPR',127,'QRR',29
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215 VEIEISD----DSKFAHFEFNGAPFTLHDDL-SILEGVR 248
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8.5%; Score 112.5; Di
Best Local Similarity 26.0%; Pred. No. 6.6;
Matches 57; Conservative 35; Mismatches
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: B90395
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandon, I.; Jeffrises, A.C.; Rozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Reference number: A99139
A;Accession: B90395
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C;Species: Caenorhabditis elegans
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Best Local Similarity 23.1%; Pred. No. 1.2; Matches 64; Conservative 46; Mismatches
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A;Molecule type: DNA
A;Residues: 1-864 <KUR>
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A;Molecule type: DNA
A;Rosidues: 1-717 <WIL>
A;Cross-references: UNIPROT:045959; EMBL:AL021493; PIDN:CAA16395.1; GSPDB:GN00023; CESP:)
A;Experimental source: clone Y51A2B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 KKAL---LOEIEKOFDDLONI-----KLRNOTLESSAENVNGIRLPFVL---VKTSRKAR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKAL---LQEIEKQFDDLQNI-----KLRNQTLESSAENVNGIRLPFVL---VKTSRKAR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Y51A2B.6b - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 Cisacession: T27067 Rimchited to the EMBL Data Library, January 1998 A;Reference number: Z20305 A;Reference number: Z20305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 -----RYEK-IKKLEEVRKELVNKIRN
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A,Introns: 8/1; 33/1
C,Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33
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A;Introns: 8/1; 33/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33
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117

4, 2005, 20:33:45

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                                                                                                                                                                                                                                                                                                                                                                                         494 D-----NDTAE------LVATEFGHTVKRVSEADVEEGFIGADDHDEHM 531
                         3 PPRG---GAAAAAAAADDITGVHILEASSVPPLPEAGGNAVQRKGAVDPDXDRKKEKAAA
                                                                                                                                  60 PRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYS--ELKSMAHIGQGFDEKNIRRVY
                                                                                                                                                                                                                                                                                              444 AVEQARVAREVVIPDVITV------QELSNRMAVRGVDIIKFLMRQGVMLKINDVI
                                                                                                                                                                                                                                                                                                                                                       178 DDLONIKLRNOTLESSAENVNGIRLPFVLVKT-----SRKARVEIE---ISDDSKFAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 EFNGAPFTL----HDDLSILEGVRRNSI--GRAGRATLH 261
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Job time : 41 secs
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A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: B70356

A;Accession: B70356

A;Residue: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1156 AQP>

A;Cross-references: UNIPROT:066878; GB:AE000699; NID:92983238; PIDN:AAC06839.1; PID:9298

A;Experimental source: strain VP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation initiation factor IF-2 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87254
R;Nierman, W.C.; Foldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. each Sci. Us.A. 98, 4136-4141, 2011
A;Reference number: A87254
A;Accession: B87254
A;Accession: B87254
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-1037 <STO>
                                                                                                                                                                                                                                     chromosome assembly protein homolog - Aquifex aeolicus
C.Species: Aquifex aeolicus
C.Jate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C.Jaccession: B70356
R.Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V. Nature 392, 353-358, 1998
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 ELSVIKCLQQLKQDSEHFQKVIQVIQKMRNLD-KDSVQNIQGI--PSVVSEFLKNLAKVR 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IKLRN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 FD-----EKNIRRRVYDAFNVLIALR--------VIAKEKKEIRWMGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                   215 VEIEISD----DSKFAHFEFNGAPFTLHDDL-SILEGVR 248
                                                                                                      ---EISDKMKENSNNKTFVMNALSFNKSDSIKSIVSSVQ 570
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8.5%; Score 112.5; DB 2;
Best Local Similarity 22.4%; Pred. No. 12;
Matches 50; Conservative 44; Mismatches 76;
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A;Gene: xcpC
C;Superfamily: chromosome segregation protein SMC1
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Best Local Similarity 22.5
Matches 63, Conservative
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anopheles
                                                                                                              (without alignments)
786.192 Million cell updates/sec
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                                                                                           4, 2005, 20:06:49 ; Search time 170 Seconds
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1 MAPPRGGAAAAATAALDLTG......SILEGVRRNSIGRAGRATLH
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Q7xe27
                                                                                                                                                                                                                                                                                                           1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                           1612378 seqs, 512079187 residues
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Q63ZR9
Q63ZR9
Q9D297
Q9D297
TDP1 MOUSE
TDP DROME
Q8ML56
Q9V6MO
Q9V6MO
TDP1 HUMAN
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Q88182
Q8LDG3
Q9ENY2
Q9ENY2
Q94VD5
Q94VD5
Q9LZE7
Q9LZE7
Q9LZE5
Q9LZE5
Q9LZE7
T0P2
T0P2
HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
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Q803N1
O44080
Q7PFI9
Q7PSH2
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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Match Length DB
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                                                                                             February
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428.5
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Maximum DB
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brachydanio
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caenorhabdi
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sulfolobus
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GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:000567; C:transcription factor activity; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003316; E2F_TDP.
InterPro; IPR00316; E2F_TDP.
Fig.; PF02319; E2F_TDP.
Fig.; PF02319; E2F_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 261 AA; 29262 MW; 5008D8F193163A28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RITGWGLREYSKIVCEKVEAKGRTTYNEVADEIXSELKSMAHIGQGFDEKNIRRRVYDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAPPRGGAAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIGQGFDEKNIRRRVYDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNIKLRNQTLESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2052804; PubMed=11108846; DOI=10.1016/S0014-5793(00)02239-0; Ramirez-Parra E., Gutierrez C.; Ramirez-Parra E., Gutierrez C.; "Characterization of wheat DP, a heterodimerization partner of the plant E2F transcription factor which stimulates E2FZDNA binding."; PEBS Lett. 486:73-78(2000).
-1- SUBCELLUIAR LOCATION: Nuclear (By similarity).
-1- SIMILARITY: Belongs to the E2F/DP family.
HSSP; Q14188; 1CF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                              DP protein.
Triticum sp.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
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Last annotation update)
                                                                                                                                                                                                                                              ALIGNMENTS
           TDP1 CAEEL
Q9GTZ7
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TDP2 MOUSE
Q9NZ54
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Q8SKS9
E2F1 HUMAN
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RA50 SULSO
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                                            09CYZ7
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Matches 258; Conservative
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 310
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R. Natire 420:112-316(2002)

C. -- SIMILBATTY: Belongs to the EZP/DP family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 -----VADEIYSELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 SSGELIVADEIFAELKSITQNGLEFDEKNIRRRVYDAFNVLIAIRVIAKDKKEIKWMGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPPRGGAAAAATAALDLTGVHILEASSVPPLPE----------AGGNAVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), Nuclear protein; Transcription; Transcription regulation 289 AA; 32157 MW; B911BEC66E3FFDAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNSIGRAG 256
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Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005667; C:transcription factor complex; IEA.
60; GO:0003700; F:transcription factor activity; IEA.
60; GO:0000074; P:regulation of cell cycle; IEA.
60; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 K--GAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRITYNE
21, Created)
21, Last sequence update)
26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%; Score 838; DB 2;
60.9%; Pred. No. 1.6e-46;
tive 31; Mismatches 36;
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InterPro; IPR009058; Wing hlx DNA bnd.
Pfam; PF02319; E2F TDP; 1.
DNA binding; Nuclear protein; Transcri
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Matches 179; Conservative
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  01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Putative DP protein.
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Q8LDG3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTYNEVADEIYSELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSN 143
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Garamens, Q84VF4; ...
Go, GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003667; E:transcription factor activity; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00915; Wing_hlx_DNA_bnd.
InterPro; IPR00915; Wing_hlx_DNA_bnd.
Pfam; PF02319; E2F_TDP; I.

DNA-binding; Nuclear protein; Transcription; Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289
                                                                                                                                                                                                                                                                               Oryža sativa (japonica cultivar-group).
Sukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNSIGRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%; Score 890.5; DB 2; Length 294; 63.1%; Pred. No. 6.5e-50; ive 31; Mismatches 36; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPPRGGAAAATAALDITGVHILEASSVPPLPE------
                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DP protein.
                                                                                                                                                               294 AA
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                                                                                                                                                                                                     Created)
                                                                                                                                                               PRT;
                          LSILEGVRRNSIGRAGRATLH 261
                                            241 LSILEGVRGNSIGKAGRATLH 261
                                                                                                                                                                                                   (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 185; Conservative
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                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=39947;
                                                                                                                                                                                                     01-JUN-2003
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Q8S182;
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RESULT 3 Q8S182 ID Q8S1 AC Q8S1

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Gaps

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36; Indels

Length 289;

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74 GDDAGSQCASGVKKKKRGQRAAGPDKTGRGLRQFSMKVCEKVESKGRTTYNEVADELVAE 133
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                                                                                                                                                                                                                                                                                                                                                                                Interro; irnovery, p. ... _ _ _ _ Transcription; Transcription regulation.
Pfam; Pf02319; Nuclear protein; Transcription; Transcription regulation.
PROTENT 385 AA; 42755 MW; 5DDB4ACA04C52AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 LEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTS
                                             DOI=10.1016/S0014-5793(00)02238-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus tremula x Populus tremuloides.
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Surosids I; Malpighiales, Salicaceae; Saliceae; Populus.
                                                                Magyar Z., Atanassova A., de Veylder L., Rombauts S., Inze D., "Characterization of two distinct DP-related genes from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bako L.S.,
                                                                                                                                                                                                                                       GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%; Score 492; DB 2; Length 385, 47.7%; Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Espinoza-Ruiz A., Saxena S., Schmidt J., Mellerowicz E.,
Bhalerao R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Espinosa-Ruiz A., Bhalerao R.P.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 PHATVEVEISEDMOLVHFDFNSTPFELHDDNFVLKTMK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Transcription factor DP1.
                                                                                                                                                    similarity) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.7%; Pred. No. 5.6e-
Matches 104; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AA
                                                                                                                              Interpro; IPR003316; E2F TDP.
Interpro; IPR009058; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                         MEDLINE=20562805; PubMed=11108847;
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                                                                                                                                                                                                                       Q14188; 1CF7.
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 LKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSE
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                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMELARITY: Belongs to the E2F/DP family.
-!- SIMILARITY: Belongs to transcription factor complex; IEA.
-- G0; G0:000074; P: regulation of factor activity; IEA.
-- G0; G0:000055; P: regulation of transcription, DNA-dependent; IEA.
-- InterPro; IPR00316; E2F_TDP.
-- InterPro; IPR00316; E2F_TDP.
-- InterPro; IPR00316; E2F_TDP.
-- InterPro; IPR003068; Wing_hix_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02119; E2F TDP; 1.
DNA-binding; Hypothetical protein; Nuclear protein; Transcription;
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation.
SEQUENCE 385 Aa; 42826 MW; A4DBDAFBD8F41D1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 RKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 PHATVEVEISEDMQLVHFDFNSTPFELHDDNFVLKTMK 291
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.3%; Score 492; DB 2; 47.7%; Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Mismatches
                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2004 (TrEMBLrel. 26,
(TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 104; Conservative
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                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                              annotation
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RESULT Q9FNY2

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346 AA; 36907 MW; 53B09A5F68F265B0 CRC64;
                                                                                                                          113; Conservative
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                                                                                                 Similarity
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nes 111;
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         SEQUENCE
                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 KKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHI-----GQGF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEKNIRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPSSRSEHAMATPASDSTFLRINHLDIHADDAAT----QDAAANKKKRGQRAVGADK-- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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InterPro; IPR003058; Wing_hlx_DNA_bnd.
Pfam; PF02319; E2F_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
         EMBL, AF181998, AAQ13675.1; -.
HSSP, Q14188; 1CF7.
GO; GO:0005667; C: transcription factor complex; IEA.
GO; GO:00007700; F: transcription factor activity; IEA.
GO; GO:0000774; P: regulation of call cycle; IEA.
GO; GO:000078; P: regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00316; Z2F TDP.
InterPro; IPR003058; Wing_hlx_DNA_bnd.
Pfam; PF02319; E2P_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 353 AA; 38444 MW; 33C9F9F440D9DEIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 APPRGGAAAATAALDLT-----GVHILEASSVPPLPEAGGNAVQRKG--AVDPDKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene; 084VD5; -. GO: 0005634; C:nucleus; IEA. GO: 00.0056634; C:nucleus; IEA. GO: 00.0005667; C:transcription factor activity; IEA. GO: 00.0003700; F:transcription factor activity; IEA. GO: 00.000074; P:regulation of cell cycle; IEA. GO: 00.000355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                      36.1%; Score 476.5; DB 2; Length 353; 42.7%; Pred. No. 5.1e-23; ive 43; Mismatches 76; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                               ,1e-23;
os 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DP TF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 HFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|| || || || :|: || HFDFNSTPFELHDDNYVLKAMK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 42.7
Matches 112, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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094V07

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                                                                                                                                                                                                                                                                                                137 PDPDNPNTPQPDEKNIRRRVYDALNVLMAMDIISKDKKEIQWKGLPR---TSMSDVEELK 193
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Gramene; Q84VA0; ...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:rucranscription factor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003116; E2F TDP.
InterPro; IPR003116; E2F TDP.
InterPro; IPR03119; E2F TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 379 AA; 40893 MW; 913F06C2975FB0CB CRC64;
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                                                                                                                                                                                                         27 APGMQGGGSAATPA-----ASASASTPASETTVARKLDGLDIQGDDAPSSQPATS
                                                                                                                                                                               52 RKKEKAAAPRIT----GWGLREYSKIVCEKVEAKGRITYNEVADEIYSELKSMAHIGQG
                                                                                                                                                                                                                                                                      107 ------FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVR
                                                                                         ------PDKD
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                                               Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                          47;
DB 2; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARVELEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNSIGRAGR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 ATVEVEISEDMQLVHFDFNSTPFELHDDSFVLK----ALGFSGK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.4%; Score 466.5; DB 2; Length ilarity 37.8%; Pred. No. 2.5e-22; Conservative 43; Mismatches 77; Indels
                                                                                       2 APPRGGAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVD--
                                            44; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
  35.7%; Score 471.5; DB 2 39.6%; Pred. No. 1.1e-22;
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Length
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%; Score 428.5; DB 2
41.3%; Pred. No. 5.2e-20;
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                                                                                                                           288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
DP-2 transcription factor-like.
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01-MAR-2001 (TrEMBLrel. 16, Created)
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les 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; T48268; T48268.
HSSP; Q14188; 1CF7.
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314 VLKTMK 319
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                                       243 ILEGVR
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Matches
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Q9FNY3
ID Q9FNY
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                          146
                                                VADEIYSELKSMAHI------GQGFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRW 138
                                                                                                MGLSNYRYEKIKKLEEVRKELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LQNI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GDDAGSQGASGVKKKKRGQRAAGPDKTGRGLRQFSMKGLISFSAPIMLSSKCLSICEKVE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AKGRITYNEVADEIYSELKSMAHIG-----QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 KLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLS 242
               207 KGLPR---TSINDIEDLQTELVGLKSRIEKKNTYLQELQDQFVGMQKLIQRNEQLYGSG-
--- DKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfan; PF02119; E2F TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                 NV--NGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGV 247
                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Weizenegger T., Bancroft I., Mewes H.W., Rudd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.6%; Score 456; DB 2; Length 413; 41.9%; Pred. No. 1.38-21; ive 41; Mismatches 68; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBMILARA LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the E2F/DP family.
-!- SIMILARITY: T48843.799.1; -.
PIR; 148364; 148364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 GNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSK------
                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                       413
                                                                                                                                                                                                                                                                                                               Name=F12E4_160;
Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR009058; Wing hlx_DNA_bnd.
Pfam; PF02319; E2F_TDP; 1.
                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15,
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Matches 103; Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 MAHIGQ-----GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
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DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 288 AA; 32560 MW; ECOAD7DC06EF92B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 VQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKS
Name=T22Pl1 60;
Arabidopsis-thaliana (Mouse-ear cress).
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0000074; P:regulation of call cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00316; E2F_TDP.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
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134 KEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESS 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 VEAKGRITYNEVADEIYSELKS----MAHIGQGFDEKNIRRRVYDAFNVLIALRVIAKEK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JUBILIARITY: Belongs to the E2F/DP family.

-1- SIMILARITY: Belongs to the E2F/DP family.

EMB1, AY50996; AAR89050.1; -..

GO, GO:0005634; C:runcleus; IEA.

GO; GO:0000567; C:rranscription factor complex; IEA.

GO; GO:00000700; F:transcription factor activity; IEA.

GO; GO:0000555; P:regulation of cell cycle; IEA.

InterPro; IPR003316; E2F_TDP.

InterPro; IPR003068; Wing_hlx_DNA_bnd.

Pfam; PF02319; E2F_TDP; 1.

DNA-binding; Nuclear protein; Transcription; Transcription regulation.

SEQUENCE 388 AA; 43155 MW; 55571AD7028BEC24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 AENV----NGIRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 LIGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                   154 EVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAEN-VNGIRLPFVLVKTSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.
Livingston R.J., Rueder M.J., Poel C.L., Chambers S.W., Schackwitz W.S.
Sherwood J.K., Sherwood A.W., Leithauser B.J., Nickerson D.A.,
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-UUL-2004 (TrEMBLrel. 27, Last sequence update) 05-UUL-2004 (TrEMBLrel. 27, Last annotation update) Transcription factor Dp-2 (E2F dimerization partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.3%; Score 399.5; DB 2
37.3%; Pred. No. 5.5e-18;
                                                                                                                                                                                               213 ARVEIEISDDSKFAHFEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                        207 AVVEIEISEDMQLVHLDFNSTPFSVHDDAXILK 239
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MSFGLESGKCSL 271
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Q6R754;
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Matches
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Q6R754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., A Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Chan M., Chang T.H., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., A Palm C.J., Quach H.L., Sakurai T., Satcu M., Southwick A., A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (MAR-2003) to the EMBL/Genannk/DDBJ databases.

L. Submitted (MAR-2003) to the EMPL/Genannk/DDBJ databases.

L. Subchitled (MAR-2013) i. Cacles 1: -

SIMILARITY: Belongs to the EZP/DP family.

R. EMBL; AJ19027; CACG45831; -

R. EMBL; AK117135; BAC41813.1; -

R. EMBL; BIO05286; AAO63350.1; -
                                                                                                                                                                                                                                                                                                                                  MEDLINE-20562805; PubMed=11108847; DOI=10.1016/S0014-5793(00)02238-9; Magyar Z., Atanassova A., de Veylder L., Rombauts S., Inze D.; "Characterization of two distinct DP-related genes from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           Aranidopsis inaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:00016874; F:ligase activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0000074; P:regulation of cell cycle; IEA.
GO; GO:0000316; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00316; BZP TDP.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DP-11ke protein (EC 6.3.2.19) (E2F dimerisation partner protein)
(DP2a) (Putative DP-2 transcription factor) (At5902470)
Name=dpa; Synonyms=At5902470/T22P11 60, dp2a;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rossignol P.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bergounioux C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation.
SEQUENCE 292 AA; 33038 MW; 644324E13561FEC5 CRC64;
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Best Local Similarity 41.3<sup>†</sup>
Matches 88; Conservative
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-!- SUBMILARITY: Belongs to the E2F/DP family.
-!- SIMILARITY: Belong to the E2F/DP family.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM DELTA), AND CHARACTERIZATION. MEDLINE-95257935; PubMed=7739537; Wu C.L., Zukerberg L.R., Ngwu C., Harlow E., Lees J.A.; "In vivo association of E2F and DP family proteins."; Mol. Cell. Biol. 15:2536-2546(1995).
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                                                                                                                    Hypothetical protein DKFZp434G222.
                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAX-2004 (TrEMBLrel. 26,
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                                                                                                                                                   Name=DKFZp434G222;
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wickernan K.J., Maramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Schwuchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rodeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y., Chellappan S.P.; "Transcription of DP transcription factors "Transcriptional activation and expression of DP transcription factors during cell cycle and TPA-induced U937 differentiation."; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB=Keratinocytes;
MEDINE=96353862; PubMed=8755520; DOI=10.1073/pnas.93.15.7594;
Rogers K.T., Higgins P.D.R., Milla M.M., Phillips R.S., Horowitz J.M.;
"DP-2, a heterodimeric partner of E2F: identification and characterization of DP-2 proteins expressed in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 62-79 FROM N.A. (ISOFORM DELTA), AND ALTERNATIVE SPLICING
                                                                                                                           Cloning and characterization of human DP2, a novel dimerization
                                                                                                                                                                                                                                                                                      TISSUE=Placenta; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Proc. Natl. Acad. Sci. U.S.A. 93:7594-7599(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SEQUENCE FROM N.A. (ISOFORM DELTA)
                          TISSUE=Kidney;
MEDLINE=95303470; PubMed=7784053;
                                                                                                                                                                                    Oncogene 10:2085-2093 (1995)
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                                                                                             ., Chellappan S.P.
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Mus musculus (Mouse)
          446 AA;
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                                         Similarity
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                                                                      Isociaciant Synonyms-48 kDa;

Isociaciant Synonyms-48 kDa;

Name=Delta; Synonyms-48 kDa;

Isociaciant Synonyms-48 kDa;

Isociaciant Synonyms-48 kDa;

Isociaciant Specificiant Synonyms-48 kDa;

Isociaciant Specificiant Synonyms in heart and skeletal muscle. Also found in placenta, kidney, brain, lung and liver. The presence as well as the abundance of the different transcripts appear to vary significiantly in different tissues and cell lines.

PTM: Phosphorylated.

SIMILARITY: Belongs to the E2F/DP family.
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Missing (In isoform Beta and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asp/Glu-rich (acidic) (NCB domain)
 Comment=Additional isoforms seem to exist. Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02319; E2F TDP; 1.
3D-structure; Activator; Alternative splicing; Cell cycle;
DNA-binding; Nuclear protein; Phosphorylation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear localization signal (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP 001353.
                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0003712; F:transcription coffactor activity; TAS.
InterPro; IPR003136; E2F TDP.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
          confirmation may be lacking for some isoforms;

Name=Alpha; Synonyms=49 kDa;

IsoId=Q14188-1; Sequence=Displayed;

Name=Beta; Synonyms=43 kDa;

IsoId=Q14188-2; Sequence=VSP_001352, VSP_001353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dimerization (Potential)
DCB1.
DCB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTIG=VSP_001354.
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/FTId=VAR_002272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
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EMBL, 19422; AAB60378.1; -.
EMBL, BC021113; AAH2113.1; -.
EMBL, U75488; AAB37321.1; -.
FMBL, 1035117; AAC50642.1; -.
PDB, LCF7; X-ray, B-121-215.
TRANSFAC; T03000; --------------------------
                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:11751; TFDP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last moncation update)
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732486C09 product:transcription factor Dp 2, full
insert sequence (Mus musculus 16 days embryo lung cDNA, RIKEN full-
length enriched library, clone:8430403A04 product:transcription factor
Dp 2, full insert sequence).
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STRAINE-STBL/GAJ; TISSUE-Lung, and Skin;
The FANTOM CONSORTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Lung, and Skin;
MEDLINE=20499374; PubMed=11042159; DoI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                   78 VEAKGRITYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENV ----NGIRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRR
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                                                                                                                                                                                                               18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CG7BL/60; TISSUE=lung, and Skin; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; RIKEN FARYOW CONSORTIUM; Frunctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                 16;
                                                                                       Length 446;
                                                                                                                                                 89; Indels
206
49236 MW; 19A6C85BAD61DFF1 CRC64;
                                                                                    29.9%; Score 394; DB 1; 37.5%; Pred. No. 1.5e-17;
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321 SFGLESGKCSL 331
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C STRAIN-GSTBL/61, TISSUB-Lung, and Skin;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hudua S., Furuno M., Hanagaki T., Haraoka T., Hirozane T.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
C -1- SIMCELLULAR LOCATION, Nuclear (By similarity).
C -1- SIMCELLULAR LOCATION, Nuclear (By similarity).
C -1- SIMLAKIY: Belongs to the EZF/DP family.
C -1- SIMLARIY: Belongs to the EZF/DP family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 CEKVQRKGTTSYNEVADELVSEFTNSNNHLAADSAYDQKNIRRRYYDALNVLMAMNIISK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLE 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 VTQTHIAEA-----AGWVPSDRKRAREFIDSDFSESKRSKKGDK-NGKGLRHFSMKV 78
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO: 00065252; F.15_SETTDP.
InterPro; IPR00316; E2F_TDP.
InterPro; IPR009068; Wing hlx_DNA_bnd.
Pfam; PF02319; E2F_TDP; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
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                                                                                                                      STRAIN=C57BL/G1 TISSUB=Lung, and Skin;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Mibal M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumino H., Akiyama J., Nishi K., Hazama M., Nishine T., Harada A., Fujiwake S., Inoue K., Takaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Tozawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.; sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:2442257; A330080J22Rik.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005667; C:transcription factor complex; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000074; P:regulation of cell cycle; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 393; DB 2; Length 385; 39.0%; Pred. No. 1.4e-17; ive 47; Mismatches 86; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #GMSFGLESGKCSL 270
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Best Local Similarity 39.0°
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Search completed: February 4, 2005, 20:33:00 Job time : 173 secs This Page Blank (uspio)

13, Appl 6, Appli 1, Appli 2, Appli 1, Appli 1, Appli 13, Appli 14, Appli

Sequence Sequence 1

Sequence

Scoring table:

Searched:

Database

Result

Title: Perfect score:

Run on:

Sequence:

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18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 33; Gaps
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GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: declaluna, Susana
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THERROF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS: 32
CORRESPONDENCE ADDRESS: 34
CITY: Arlington 5859199th Glebe Rd. 8th floor
CITY: Arlington 5859199th Glebe Rd. 8th floor
CITY: Arlington 5859199th Glebe Rd. 8th floor
CITY: Arlington 5859199th Glebe Rd. 8th floor
CONDUTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PRELETIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFRCATION NUMBER: GB 9610195.1
FILING DATE: 15-MAX-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawdord, Arthur R.
REGISTAMION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION NUMBER: 117-220
TELECOMMUNICATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION NOM FOR TON NO 6:
TELEPHONE: 703-816-4100
TELEPHONE: 703-816-4100
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TELEPHONE: 703-816-4100
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                                                                                                                                                                                                                                                                                                                                                                                                              US-09-248-796A-21863
US-09-640-211A-1167
                                                                                            US-08-723-415B-13
US-08-81-814A-6
US-08-81-092-1
US-09-189-677A-13
US-09-242-737-2
US-09-215-113-1
US-09-710-861-13
US-08-139-937-14
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US-07-882-711-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 370 amino acids
amino acid
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-08-723-415B-6
Sequence 2, Appli
Sequence 9220, Ap
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, Appli
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2, Appli
11, Appli
11, Appl
11, Appl
10, Appl
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Sequence 8808, Ap
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Sequence 1056, Ap
Sequence 10, Appl
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Sequence 1031, Ap
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1319
1 MAPPRGGAAAATAALDLTG.....SILEGVRRNSIGRAGRATLH 261
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Sequence 2,
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Sequence 11
Sequence 11
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Re_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-189-627A-2
US-09-189-627A-4
US-09-189-627A-4
US-09-189-627A-4
US-09-199-627A-4
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US-08-723-415B-11
US-09-189-627A-11
US-09-189-627A-11
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S-09-078-596-2

S-09-189-627A-11

S-09-710-861-11

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Maximum Match 100%
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TYPE: PRT
ORGANISM: mouse
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                            VEAKGRITYNEVADEIYSELKS----MAHIGGGFDEKNIRRRVYDAFNVLIALRVIAKEK 133
                                          134 KEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESS 193
                                                                                                 194 AEN---VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                        28 VTQTHIABAA------GWVPSKRSKKGDK-----NGKGLRHFSMKVCEK 65
                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09189627A

Sequence 6, Application US/09189627A

Sequence 6, Application US/09189627A

Sequence 6, Application US/09189627A

SERENCE INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: de la Luna, Susana

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION UNMBER: US/09/189,627A

CURRENT APPLICATION NUMBER: 08/723,415

PRIOR PILING DATE: 1996-09-15

PRIOR FILING DATE: 1996-09-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0
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; Pred. No. 4.7e-29;
51; Mismatches 74; Indels 33
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Patent No. 389769
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
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244 MSFGLESGKCSL 255
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244 MSFGLESGKCSL 255
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Best Local Similarity
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US-09-189-627A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Gaps
APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
CURRENT APPLICATION NUMBER: US/09/110,861
CURRENT APPLICATION NUMBER: US/09/110,861
CURRENT FILING DATE: 1208-11-13
PRIOR PILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-09-30
PRIOR PILING DATE: 1996-05-15
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOY: 2.0
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JOS-08-723-15B-8

JOS-08-723-15B-8

JOS-08-723-15B-8

JOS-08-723-15B-8

JOS-08-723-15B-8

JOS-08-723-110N:

APPLICANT: LaThangue, Nicholas B.

APPLICANT: deLaluna, Susana

APPLICANT: deLaluna, Susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 21

CORRESPONDENCES: 21

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NO. 5859199th Glebe Rd. 8th floor

CITY: Arlington

STATE: WA

COUNTRY: USA

COMPUTER: USA

ZIP: 22201-4741

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PAPELING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATALING

APPLICATION NUMBER: US/08/723,415B

FILING DATE: 15-MAY-1996

FILING DATE: 15-MAY-1996
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37.3%; Pred. No. 4.7e-29;
tive 51; Mismatches 74;
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Best Local Similarity 37.34
Matches 94; Conservative
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244 MSFGLESGKCSL 255
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                                                                                                                                                                                                                     192 SSAEN --- VNG-IRLPPVLVKTSRKARVEIEISDDSKFAH - FEFNGAPFTLHDDLSILEG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 SSAEN---VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEG 246
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79 CEKVORKGTTSYNEVADELVSEFTNSNNHLAADSAYDQENIRRRVYDALNVLMAMNIISK 138
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Sequence 8, Application US/09710861

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: La Thangue, Nicholas

ITILE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REPERENCE: 620-54

CURRENT APPLICATION NUMBER: US/09/710,861

CURRENT FILING DATE: 2000-11-13

FRIOR APPLICATION NUMBER: US/09/189,627

FRIOR FILING DATE: 1998-11-10

FRIOR FILING DATE: 1998-11-10

FRIOR PRILING DATE: 1996-09-30

FRIOR FILING DATE: 1996-09-30

FRIOR FILING DATE: 1996-09-15

SOFTWARE: PATENTON NUMBER: GB 9610195

FRIOR FILING DATE: 1996-05-15

NUMBER OF SEQ ID NOS: 25

SEO ID NO 0. SEQ ID NOS: 20
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APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       257 MGMSFGLESGKCSL 270
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257 MGMSFGLESGKCSL 270
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Best Local Similarity 38.64
Matches 98; Conservative
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APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Susana
ITILE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
ITILE OF INVENTION: UNMBER: US/09/189,627A
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1996-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-05-15
PRIOR PILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Gaps
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                              NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-189-627A-8
; Sequence 8, Application US/09189627A
; Patent No. 6159691
                                                                                                                                                                                                             TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 385 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 VRRNSIGRAGRATL 260
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 38.67
Marches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-723-4158-8
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Best Local Similarity
Matches 98; Conserv
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ORGANISM: mouse
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PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 961
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 446
TYPE: PRT
CORGANISM: mouse
US-09-189-627A-2
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                                                                                                                                                                                                                                                            Local Similarity
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US-09-710-861-2
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US-09-710-861-2
                                                                                                                                                                                                                                          Query Match
Best Local S:
Matches 98
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Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT APPLICATION NUMBER: 08/723,415
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                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-58P-1996
CLASSITCATION: 435
PRIOR APPLICATION NUMBER: GB 9610195.1
APPLICATION NUMBER: GB 9610195.1
RILING DATE: INFORMATION:
NAME: CTAMFORM ATHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELEPRATION NUMBER: 25,327
TELEPRATION NUMBER: 117-220
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
TELEPRATION NUMBER: 107-320
                             NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: UXXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
         HILE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 VRRNSIGRAGRATL 260
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                                                                                                         CITY: Arlington
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-189-627A-2
                                                                                                                                                               COUNTRY:
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                                                                                                                                                    89 VTQTHIAEA-----AGWVPSSRKRAREFIDSDFSESKRSKKGDK-NGKGLRHFSMKV 139
                                                                                                                                                                                                                   75 CEKVEAKGRITYNEVADELYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09710861
; Sequence 2, Application US/09710861
; Patent No. 6387649
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION PACTOR DP-3 AND ISOFORMS THEREOF
; FILE REPRENCE: 620-61
; CURRENT APPLICATION NUMBER: US/09/110,861
; CURRENT FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: US/09/189,627
; PRIOR APPLICATION NUMBER: US/09/33,415
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR APPLICATION NUMBER: GB 9610195
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 2
: LENGTH: 446
                                                                                                            18 LTGVHILEASSVPPLPEAGGNAVQRKGA---VDPDKDRKKEKAAAPRITGWGLREYSKIV
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29.5%; Score 389; DB 3; Length 446;
Best Local Similarity 38.6%; Pred. No. 6.9e-29;
Matches 98; Conservative 48; Mismatches 86; Indels 2
     Length 446;
                                                         86; Indels
29.5%; Score 389; DB 3; 38.6%; Pred. No. 6.9e-29; tive 48; Mismatches 86.
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NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-220
TELEPRONICATION INFORMATION:
TELEPRONE: 703-816-4100
                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 14-01
                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 37.5
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                  COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-189-627A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                          Sequence 9220, Application US/09949016
Fatent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
                      192 SSAEN---VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FBFNGAPFTLHDDLSILEG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLE 191
                                                                                                   260 QQNGGPPAVNSTIQLPFIIINTSRKTVIDCSISSD-KFEYLFNFDNT-FEIHDDIEVLKR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 DEIYSEL-KSMAHIG--QGFDEKNIRRRYYDAFNVLIALRVIAKEKKEIRWMGLSNYRYE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 KIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 FVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRRNSIGRAGRATL 260
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Patent No. 5859199
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.2%; Score 385; DB 4; Length 331; 38.7%; Pred. No. 1.1e-28; tive 48; Mismatches 84; Indels 1
                                                                                                                                                       247 VRRNSIGRAGRATL 260
                                                                                                                                                                                               318 MGMSFGLESGKCSL 331
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Best Local Similarity
Matches 92; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
                                                                                                                                                                                                                                                           RESULT 10
US-09-949-016-9220
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LENGTH: 331
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US-08-723-415B-4
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78 VEAKGRTTYNEVADEIYSEL-KSNAHIG--QGPDEKNIRRRVYDAFNVLIALRVIAKEKK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09189627A

Sequence No. 6159691

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: de la Luna, Susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REFERENCE: 620-54

CURRENT FILING DATE: 1998-11-10

PRIOR PELICATION NUMBER: 08/723,415

PRIOR PELICATION NUMBER: 08/723,415

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.1%; Score 384; DB 2; Length 369; 37.5%; Pred. No. 1.6e-28; tive 50; Mismatches 75; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-52P-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
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50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GFDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 QGPPAVNSTIQLPFIIINTSRKTVIDCSISSD-KFEYLFNFDNT-FEIHDDIEVLKRMGM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 17; Gaps
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: defaluma, Susana
APPLICANT: defaluma, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: REALBLE FORDY disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
28.7%; Score 378.5; DB 2;
Best Local Similarity 42.4%; Pred. No. 6.2e-28;
Matches 87; Conservative 41; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 DSKFAH-FEFNGAPFTLHDDLSILE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | || : | |: | :|||: :|:
D-KFEYLFNFONT-FEIHDDIEVLK 301
                                                                                                                                                                  RESULT 14
10S-08-723-415B-11
5 Sequence 11, Application US/08723415B
7 Patent No. 5859199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 11:
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                                                     250 NSIGRAGRATL 260
                                                                               : :|: :|
244 SFGLESGKCSL 254
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ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arlington
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CITY: An
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 VEAKGRITYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
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                                                                                                                                                                                                                                                                                                       78 VEAKGRITYNEVADEIYSEL-KSMAHIG--QGFDEKNIRRRVYDAFNVLIALRVIAKEKK 134
                                                                                                                                                                                                                                                                                                                            66 VQRKGTISYNEVADELVSEFINSNHILAADSAYDQENIRRRYYDALNVI,MAMNIISKEKK 125
                                                                                                                                                                                                                                                                                                                                                                                        135 EIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKOFDDLONIKLRNOTLESSA 194
                                                                                                                                                                                                                                                                                                                                                                                                                    195 EN---VNG-IRLPFVLVKTSRKARVEIEISDDSKFAH-FEFNGAPFTLHDDLSILEGVRR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 QGPPAVNSTIQLPFIIINTSRKTVIDCSISSD-KFEXLENFDNT-FEIHDDIEVLKRMGM 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 VIQTHIAEAA.-----GWVPSKRSKKGDK------NGKGLRHFSMKVCEK 65
                                                                                                                                                                                                                                             28 VIQTHIAEAA------GWVPSKRSKKGDK-----NGKGLRHFSMKVCEK 65
                                                                                                                                                                                                               18 LTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKIVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/710,861
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR PILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-09-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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                                                                                                                           29.1%; Score 384; DB 3; Length 369; 37.5%; Pred. No. 1.6e-28;
                                                                                                                                                                         50; Mismatches
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US-09-710-861-4
; Sequence 4, Application US/09710861
; Patent No. 6387649
                                                                                                                                                                         94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 SFGLESGKCSL 254
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Best Local Similarity
Matches 94; Conserva
                                                                                                                             Query Match
Best Local Similarity
Matches 94; Conserv
                  LENGTH: 369
TYPE: PRT
ORGANISM: mouse
                                                                               US-09-189-627A-4
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50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.7%; Score 378.5; DB 2; Length 410; Best Local Similarity 42.4%; Pred. No. 6.2e-28; Matches 87; Conservative 41; Mismatches 60; Indels 17
US-08-428-131-2

Sequence 2, Application US/08428131

Sequence 2, Application US/08428131

Sequence 2, Application US/08428131

Sequence 2, Application US/08428131

GENERAL INFORMATION:
TITLE OF INVENTON: Transcription Factor DP-1

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Nature & Vanderhye

STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STRYE: Virgina

CONDTRY: U.S.A.
ZIP: 22201-4714

COMPUTER: ISM PC Compatible
OCMPUTER: ISM PC Compatible
OCMPUTER: ISM PC Compatible
OCMPUTER: ISM PC Compatible
OCMPUTER: DatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
CASSIFICATION NUMBER: US/08/428,131

FILING DATE: 23-UN-1995

CLASSIFICATION NUMBER: US/08/428,131

FILERPONENCE TOWNER: US/08/1100

INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LERKGTH: 410 anino acid
TYPE: amino acid
TYPE: amino acid
TYPE: TOWNEY: LIBERT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 4, 2005, 20:34:32
Job time: 44 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 D-KFEYLFNFDNT-FEIHDDIEVLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-428-131-2
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February 4, 2005, 20:33:05; Search time 132 Seconds (without alignments) 644.003 Million cell updates/sec
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1 MAPPRGGAAAAATAALDLTG......SILEGVRRNSIGRAGRATLH 261
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(cgn2_6/ptodata/2/pubpaa/us09C_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	* Query Match	* Query Match Length DB	DB	ID	Description	
	842	63.8	!	16	US-10-437-963-136371	Sequence 136371.	
8	464	35.2		15	US-10-425-114-46555	Sequence 46555, A	
٣	453.5			15	US-10-424-599-186648	Sequence 186648,	
4	438			15	US-10-424-599-185947	Sequence 185947,	
S	374.5			14	US-10-106-698-4846	Sequence 4846, Ap	
9	374	28.4		16	US-10-767-701-49206	Sequence 49206, A	
7	372.5	28.2		16	US-10-437-963-166158	Sequence 166158,	
80	361	27.4		15	US-10-425-114-36974	Sequence 36974, A	
Ø,	354	26.8		0	US-09-220-091-7	Sequence 7, Appli	
10	342.5	26.0	207	15	.5 US-10-425-114-71403	Sequence 71403, A	
11	337.5			16	US-10-437-963-167076	Sequence 167076,	
12	299.5			14	US-10-053-248-24	Sequence 24, Appl	
13	299.5			16	US-10-345-837~24	Segmence 24. Appl	

	Sequence 95, Appl Sequence 8, Appli Sequence 2, Appli
15 · US-10-424-599-234773 14 · US-10-214-188-10 15 · US-10-314-188-10 16 · US-02-900-147-1 15 · US-10-282-122A-46532 15 · US-10-282-122A-4534 15 · US-10-389-56-435 15 · US-10-389-56-435 15 · US-10-389-56-692 15 · US-10-389-56-692 16 · US-10-389-56-692 17 · US-10-389-56-692 18 · US-10-389-56-692 19 · US-09-842-484A-2 10 · US-09-842-484A-3 14 · US-10-17-613-8 15 · US-10-217-613-8 16 · US-09-22-091-9 17 · US-09-22-091-9 18 · US-10-217-613-8 19 · US-09-22-091-9 15 · US-09-22-091-9 16 · US-09-23-13626 17 · US-09-23-13626 18 · US-09-23-13626 19 · US-09-23-13626 19 · US-09-23-13626 19 · US-09-23-13626 19 · US-09-23-13626 19 · US-09-23-114-71965 19 · US-09-17-613-8 19 · US-09-17-613-8 19 · US-09-17-613-8 19 · US-09-17-613-8 19 · US-09-17-613-8 19 · US-09-17-17-18-9	14 US-10-326-185-95 15 US-10-309-560-8 16 US-10-642-248-2
11156 11156 11156 11156 11156 11156 11156 1157 1158 1159 1159 1159 1159 1159 1159 1159	972 972 1
1111 1111 112 113 113 113 113 113 113 11	7.7 7.7
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## ALIGNMENTS

RESULT 1 US-10-437-963-136371, A Sequence 136371, A Publication No. US GENERAL INFORMATIO APPLICANT: La Ros APPLICANT: Zhou, APPLICANT: Zhou, APPLICANT: Barba APPLICANT: Boukh APPLICANT: Barba	SULT 1 1-10-437-963-136371 1-10-437-963-136371 Subjuction No. US20040123343A1 Subjuction No. US20040123343A1 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Mu, Wei APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad
TITLE OF INVENT: TITLE OF INVENT: FILE REPERENCE: CURRENT APPLICA CURRENT APPLICA CURRENT APPLICA SEQ ID NO 136371 LENOTH: 369 TYPE: PRT ORGANISM: OFYZ	ATTILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPRENCE: 38-21 (53221)B CURRENT APPLICATION UNMER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 EQ ID NOS: 204966 TYPE: PRINCE DATE: ACID MOS: 204966 TYPE: PRINCE ORGANISM: OFYZA SATIVA
OTHER INFORMATIO US-10-437-963-136371 Query Match Best Local Similar Matches 185; Con	OTHER INFORMATION: Clone ID: PAT_MRT4530_37957C.1.pep -10-437-963-136371 Query Match Best Local Similarity 50.4%; Pred. No. 2e-66; Matches 185; Conservative 32; Mismatches 36; Indels 114; Gaps 5;
o S	1 MAPPRGGAAAATAALDLIGYHILEASSVPPLPE
δλ	35AGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYSKI 73

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TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 EGVR 248
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258 KAMK 261
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US-10-424-599-185947
                                                              -10-424-599-186648
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APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
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61 KKSVSLRSGGGGNAAEREEGGA---NRNGKKEKTGAQRITGWGLREFSKIGFTKLPGPGL 117
                                                                                                                                      118 SRPGGKHSYCAEVTAVFTLPYPGGKPGNRGNRAVTGGMVNPGVDCFVSKKVEAKGRTTYN 177
                                                                                                                                                                                                                           98 E------VADEIYSELKSMAHIGQGFDEKNIRRRVYDAFNVLIALRVI 129
                                                                                                                                                                                                                                                                  130 AKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQT 189
                                                                                                                                                                                                                                                                                                                                                                                    190 LESSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 SQRPAESVNGILLPFLLIKTSRKARVEIEISEDSKFARFDFNGAPFTWHDDVSILEAIRR 357
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                                                                                                     -----VCEKVEAKGRTTYN
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US-10-425-114-46555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46555, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSIGRAG 256
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ORGANISM: Zea mays
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US-10-425-114-46555
                                                                                              74 ----
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Sequence 185947, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Boy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules
TITLE REPERBENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 185947
LENGTH: 314
Sequence 186648, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBNGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 RNQTLESSAENVNG-IRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSIL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 KIVCEKVEAKGRITYNEVADEIYSELKSMAHI-----GQGFDEKNIRRRVYDAFNVLIAL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 RVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIE-KQFDDLQNIKL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:|| ::| | ::| | ||::| 21 NSLPPPVDKTILKLNHLDVHADDAGSHASLASG---KKKKRGGGRAVGPDKSGRGLRQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 SSVPP------LPEAGGNAVQRKGAVDPDKDRKKEKAAAPRITGWGLREYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15; Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_139556C.1.pep
US-10-424-599-186648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.4%; Score 453.5; DB 15; Best Local Similarity 42.6%; Pred. No. 6.5e-32; Matches 104; Conservative 42; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(320)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
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Squence 166158. Application US/10437963

Squence 166158. Application US/10437963

Squence 166158. Application No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 166158

LENGHIA: 318
                                                                                                                                                                                            RESULT 6
US-10-767-701-49206
; Sequence 43206, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Exou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (5535) B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 49206
; LENGTH: 120
                           225 KQSQLQELILQQIAFKNLVQRNRHAEQQASRPPPPNSVIHLPFIIVNTSKKTVIDCSISN 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 WMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENV 197
  166 KKALLQEIEKQFDDLQNIKLRNQTLESSAENV----NGIRLPFVLVKTSRKARVEIEISD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 WACL-HFQYEYI-KLESTRKELMIRVKNKKKLLQEIERQFDDLQNIKFRNQLLQRPAESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NGICLPFLLVKASRKARVBIBISBNSKPAGFDFNCTPFTLHDDVSILEAIRCNN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 NGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVRRNS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: LIB3476-039-P1-K1-D2.pep
US-10-767-701-49206
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US-10-437-963-166158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.4%; Score 374; DB 16; Best Local Similarity 67.5%; Pred. No. 2e-25; Matches 77; Conservative 17; Mismatches 18;
                                                                                        222 DSKFAH-FEFNGAPFTLHDDLSILE 245
                                                                                                                    285 D-KFEYLFNFDNT-FEIHDDIEVLK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.2%;
Best Local Similarity 37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-437-963-166158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (351)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE
LOCATION: (352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (342)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSM-AHI---GQ 105
                                                                                                                                                                                 54 KKRGGQRAGGPDKSGRCLRYFSMKVCEKVESRGRRSYNEVADELVAEFADPINGVSTPDQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 KDRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAH----IG 104
                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-4846
                                                                                                                                                                                                                                                105 QGPDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIR 164
                                                                                                                                                                                                                                                                                                                                      165 NKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLVKTSRKARVEIEISDDS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.4%; Score 374.5; DB 14; Length 355;
42.0%; Pred. No. 8.1e-25;
tive 42; Mismatches 60; Indels 17; Gaps
                                                                                                               9
                                                                 Length 314;
                                                                                                               66; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138923C.1.pep
US-10-424-599-185947
                                                              33.2%; Score 438; DB 15;
45.9%; Pred. No. 1.5e-30;
tive 39; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                               224 KFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 QLVHFDYICAPFEMHDDNYVLKAMK 258
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Best Local Similarity 42.0%
                                                                                                           94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                            Query Match
Best Local Similarity
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-220-091-7
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Best Local Similarity 41.39
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||| ||:
228 IHDDFEILK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 LHDDLSILE 245
                                                                                                                                                                                          SEQ ID NO 7
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APPLICANT: Zhou, Yihua
APPLICANT: Scvalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILING DATE: 20153113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 36974
LENGTH: 222
TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 VADEIYSELKSMAH----IGQGFDEKNIRRRYYDAFNVLIALRVIAKEKKEIRWMGLSN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ------FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVR 156
                                                                                                                                                                                                                137 PDPDNPNTPQFDEKNIRRRVYDALNVLMAMDIISKDKKEIQWKGLPR---TSMSDVEELK 193
                                                                                                                                                                                                                                                                      157 KELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENVN-GIRLPFVLV---- 207
                                                                                                                                                                                                                                                                                               51
                                                                        27 APGMQGGGSAATPA-----ASASASTPASETTVARRLDGLDIQGDDAPSSQPATS 76
                                   2 APPRGGAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVD------PDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFTLHDDLSILEGVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3170-045-C12_FLI.pep
US-10-425-114-36974
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-10-425-114-36974
Sequence 36974, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09220091
Patent No. US20020064523A1
GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz
APPLICANT: Craig Ceol
APPLICANT: Xiaowei Lu
                                                                                                                                                                                                                                                                                                                                                         208 ----KTSRKARVEIEIS 220
                                                                                                                                                                                                                                                                                                                                                                                            254 LAKNOMIŘKPGLÉMĚVŠ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.4%;
Best Local Similarity 46.4%;
Matches 77; Conservative 3
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-220-091-7
  Matches
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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 207

TYPP: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 QGFDEKNIRRRYYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELV---N 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 GLRHFSTKVCEKVKEKGLTNYNEVADELVADYFQNNLIKQIDVVKQEYDMKNIRRRVYDA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 FNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNKKALLQEIEKQFDD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 LONIKLRNOTLE---SSAENVNGIRLPFVLVKTSRKARVEIEISDDSKFAHFEFNGAPFT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 YKNLVERNRKNEHKNGRPENDTVLHLPFLIINTDKEANVECSVSSDKSEFLFSFD-KKFE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GLREYSKIVCEKVEAKGRITYNEVADEIYSE-----LKSMAHIGOGFDEKNIRRRVYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 17; Gaps
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Best Local Similarity 44.4%; Pred. No. 2.7e-22;
Matches 75; Conservative 29; Mismatches 48; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                              26.8%; Score 354; DB 9; Length 575; 41.3%; Pred. No. 1e-22; tive 34; Mismatches 67; Indels
TITLE OF INVENTION: A TUMOR SUPPRESSOR PATHWAY IN C. ELEGANS FILE REFERENCE: 01997/202003
CURRENT APPLICATION NUMBER: US/09/220,091
CURRENT FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: 60/047,996
EARLIER PILING DATE: 1997-05-28
EARLIER PILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASELSQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE119B07_FLI.pep
US-10-425-114-71403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays subsp. mexicana
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51 DRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRTTYNEVADEIYSELKSMAHIG----QG 106
                                                                                                                                                                                                                                                                                                                                                                                 107 FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNK 166
                                                                                                                                                                                                                                                                                    167 KALLQEIEKQFDDLQNIKLRNQTLESSAEN----VNGIRLPFVLVKTSRKARVEIEISDD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 DRKKEKAAAPRITGWGLREYSKIVCEKVEAKGRITYNEVADEIYSELKSMAHIG----QG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 FDEKNIRRRVYDAFNVLIALRVIAKEKKEIRWMGLSNYRYEKIKKLEEVRKELVNKIRNK 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 QSELQQLILQQIAFKNLVLRNQYVEEQVSQRPLPNSVIHVPFIIISSSKKTVINCSISDD 274
                                                                                                                       Gaps
                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.7%; Score 299.5; DB 16; Length 405; Best Local Similarity 33.7%; Pred. No. 4.6e-18; Matches 68; Conservative 47; Mismatches 72; Indels 15;
                                                                      DB 14; Length 405;
                                                                    ch 22.7%; Score 299.5; DB 14; Length
1 Similarity 33.7%; Pred. No. 4.6e-18;
68; Conservative 47; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-345-837-24

Sequence 24, Application US/10345837

Publication No. US20040137440A1

GENERAL INFORMATION:

APPLICANT: Lin, Biaoyang

TITLE OF INVENTION: Androgen Regulated Nucleic Acid

TITLE OF INVENTION: Androgen Regulated Nucleic Acid

TITLE OF INVENTION: Molecules and Encoded Proteins

FILE REFERENCE: P-IS 5589

CURRENT APPLICATION NUMBER: US/10/345,837

CURRENT FILING DATE: 2003-01-15

PRIOR FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 234773, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION: A APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 SKFAHFEFNGAPFTLHDDLSIL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 KSEYLFKFNSS-FEIHDDTEVL 295
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275 KSEYLFKFNSS-FEIHDDTEVL 295
; ORGANISM: Homo sapiens
US-10-053-248-24
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US-10-345-837-24
                                                                    Query Match
Best Local Similarity
Matches 68; Conserval
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US-10-424-599-234773
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21 (5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 RINDLDIHGDDAPSSQAPTSKKKKRGARAVGPDKGGRGLRQFSMKVCEKVESKGRTTYNE 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 --------QQYDEKNIRRVYDALNVLMAMEIISKDKKEIQWKGLPR---TS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 IKKLEEVRKELV---NKIRNKKALLQEIEKQFDDLQNIKLRNQTLESSAENV--NGIRLP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 -------DKDRKKEKAAAAPRITGWGLREYSKIVCEKVEAKGRITYNE
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                        Ouery Match 25.6%; Score 337.5; DB 16; Length 263; Best Local Similarity 35.5%; Pred. No. 1.1e-21; Matches 97; Conservative 33; Mismatches 56; Indels 69;
  ----RNSIGRAGRAT 259
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US-10-053-248-24
; Sequence 24, Application US/10053248
; Publication No. US20030144188A1
; Publication No. US20030144188A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Blaoyang
; TITLE OF INVENTION: Androgen Regulated Nucleic Acid
; TITLE OF INVENTION: Molecules and Encoded Proteins
; FILE REFERENCE: P-IS 4814
; CURRENT APPLICATION NUMBER: US/10/053,248
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 34
; SEC ID NO 24
; SEC ID NO 24
; LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_65721C.1.pep
US-10-437-963-167076
221 DDSKFAHFEFNGAPFTLHDDLSILEGVR-
                                                                                                                                                            Sequence 167076, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                 Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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ORGANISM: Oryza sativa
                                                                                                                                                                                                        GENERAL INFORMATION:
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us-10-088.

"TILL OF PERICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yingwei

TITLE OF INVENITION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENITION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 234773

LENGTH: 165

TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPPRGGAAAATAALDLTGVHILEASSVPPLPEAGGNAVQRKGAVDPDKDRKKEKAAAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 39.9%; Pred. No. 5.2e-12;
Matches 55; Conservative 20; Mismatches 40; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: U.S.A...
COUNTY: U.S.A...
COUNTY: U.S.A...
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: CURNOWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/10214188
; Publication No. US20030022260A1
GENERAL INFORMATION:
HIDMANDS, RENB
HIDMANDS, RELEANORE M.
TITLE OF INVERTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSE:
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_54029C.1.pep
US-10-424-599-234773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEI, AND THE SOLVE THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T
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SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
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148 VYDALNVLMAMDIISKDK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 VYDAFNVLIALRVIAKEK 133
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                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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US-10-214-188-10
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74 VCEKVEAKGRITYNEVADEIYSELKSM-AHI---GQGFDEKNIRRRVYDAFNVLIALRVI 129
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                              DB 14; Length 74;
                                                                                                                                                          Query Match
15.4%; Score 203.5; DB 14; Length
Best Local Similarity 58.3%; Pred. No. 1.6e-10;
Matches 42; Conservative 13; Mismatches 12; Indels
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 4, 2005, 20:45:29
Job time : 134 secs
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63 SKEKKEIKWIGL 74
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OM protein

Run on:

Sequence:

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AX449314 Sequence
BY005286 Arabidops
AX44932 Sequence
AX117135 Arabidops
AX44929 Sequence
AX774250 Sequence
AX774251 Sequence
AX774251 Sequence
AX774251 Sequence
AX774251 Sequence
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AX774251 Sequence
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AX77426 Sequence
L40386 Human DP-2
CQ44960 Sequence
L40386 Human DP-2
CQ44960 Sequence
AX33694 Sequence
AX31698 Sequence
AX72088 Sequence
AX72088 Sequence
AX72088 Sequence
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                     Populus t
Populus t
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AR029043 Sequence AR120686 Sequence
AR210076 Sequence
AX003677 Sequence AX003677 Sequence 3
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Gutierrez-Armenta,C.C. and Ramirez-Parra,E.C.
Gutheat dp proteins and uses thereof
Patent: WO 0121644-A 1 29-MAR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
LOCATION/QUALIfiers
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/organism="Triticum monococcum"
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20. .805
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ATH319027
AX449297
                                                                                       AX449314
AY224589
AX449342
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AR029045
AR120688
AR210078
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AR120689
AR210079
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AR380911
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CQ489116
CQ494960
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AX100704
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   Command line parameters:
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-UNITS=bits -START=1 -END=-1 -MATRIX=bicombc -TRANS=human40.cdi -LIST=45
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-UNITSMT=ptc -NORM=sext -HEAPSIZE=500 -MINLENE=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AJ271917 Triticum
AY224529 Oryza sat
AK111611 Oryza sat
                                                                                                                     6, 2005, 20:16:37; Search time 4657 Seconds (without alignments) 2715.656 Million cell updates/sec
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1 MAPPRGGAAAAATAALDLTG......SILEGVRNSIGRAGRATLH 261
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                   - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AY224529
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Jatabase :

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Query Match:
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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       PLN
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Gutierrez,C.
Direct Submission
Submitted (03-FEB-2000) Gutierrez C., C.S.I.C.-U.A.M.,
Biologia Molecular, Cantoblanco, Madrid 28049, SPAIN
Location/Qualifiers
           linear
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Indels:
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Triticum sp.
Triticum sp.
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/gene="dp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCGCCTCCCTGCGGCGATGCCGCGGCGGCTGCCTCCGCCGCGCCCGGCCTACCAAC
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  /db_xref="taxon:39947"
/note="derived from yeast two-hybrid experiments"
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Matches:
Conservative:
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Indels:
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AY224529.1 GI:29367574
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaae; Oryzaa.

1 (bases 1 to 885)

Clooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P.,

Ellero, C., Goff, S.A. and Glazebrook, J.

Identification of rice (Oryza sativa) proteins linked to the cyclin-mediated regulation of the cell cycle
                                                                                100
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                                                                                                                                                                                                                                                                                                                                                                                           160
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AlaHisIleGlyGlnGlyPheAspGluLysAsnIleArgArgArgValTyrAspAlaPhe
                                                                                                                                                                                                                                                                                                                   LeuSerAsnTyrArgTyrGluLysIleLysLysLeuGluGluValArgLysGluLeuVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTCAAATTACAGATATGAAAAATAAAGAAGCTTGAGGAAGTTCGTAAAGAACTCGTC
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                                                                             LysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSerMet
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Ellero, C., Goff, S. and Glazebrook, J.
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION ACCESSION VERSION

AY224529 LOCUS

RESULT 3

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FEATURES

TITLE JOURNAL

MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 GCGGCTGGTCCAGATAAGACTGGAAGAGGACTACGTCAATTTAGTATGAAAGTTTGTGAA 339
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520 GATABABABABATTCBATGGAGAGGGGTCTTCCTCGGACBAGGTTAAGCGACATTGAAGAA 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ileArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 GluiysiysgluileArgTrpMetGlyieuSerAsnTyrArgTyrGluiysIleLysLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7. SerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeuValLysThrSer
|||||||
| AGCTCAGGAATGCTCCCAGTGGGGGGTGTTGCTCTTTTATCCTTGTCCAGACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLy8IleValCy8Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGlu
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                                                                                                                                                function = "cell cycle regulation"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                   /protein id="CAC15484.1"
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492.00
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47.71%
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/gene="dpb"
1. .1158
/gene="dpb"
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Query Match:
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Submitted (06-SEP-2000) Magyar Z., Department Plantgenetica,
Laboratorium voor Genetica, Universiteit Gent, K.L. Ledeganckstraat
35., B-9000, Gent, BELGIUM
Location/Qualifiers
1..1158
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Prilke protein; dpb gene.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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ATH294532 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 5

REFERENCE AUTHORS TITLE

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FEATURES

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Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent this set was done by comparison with known proteins: two percent the clones are estimated to be 5-truncated; less than one percent are 3.-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5-truncated if it lacks the translation initiation start (ARG). A sequence is considered to be 3'-truncated if it lacks the croneded protein. Please note that these cDNA sequences are derived from the Ws or Laber ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. Genset carried out the library production and sequence assembly.

S' sequences, selection of clones, and sequence assembly.
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alnvlaand iskokkei gorgleptsls. Bifelknerlslenn iskktavsgeleeg
vvglonlignbehlyssgnabsggvalpptivuqtrehatveveisedmolydfnst
ppellhonfulktmkrcooppooppigonsglvchiftpengtveveisedmolydfnst
thlosoohoohsolotipmyssadtapvksellnn
                                                                                                                                                  AYOB6018 11618 bp mRNA linear PLN 14-APR-2003
Arabidopsis thaliana clone 206791 mRNA, complete sequence.
                                                                                                                                                                                                                                                                                                     Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
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Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldman, K.
Full-Length cDNA from Arabidopsis thaliana
Unpublished
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Feldmann, K.
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N. Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
                        AsnGlyAlaPropheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248

    1618 /organism="Arabidopsis thaliana"

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db_xref="G1:21554147"
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Arabidopsis thaliana (thale cress)
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Alignment Scores:

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1640 bp mRNA linear PLN 31-DEC-2003
Populus tremula x Populus tremuloides transcription factor DP1
(DP1) mRNA, complete cds.
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TTTGCACTTCCAAATAACGATGGAACATCCCCTGATCAGCAACAGTATGATGATGAAAAAC
                                                                                                                                37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
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                             Conservative:
Mismatches:
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Unpublished
   Length:
Matches:
                                                           Indels:
                                                                                                      US-10-088-830-2 (1-261) x AY086018 (1-1618)
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Bhalerao, R.P. and Sandberg, G.
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta, Magnolophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

1 (bases 1 to 1640)

2 (Bases 1 to 1640)

3 Espinosa-Raiz,A., Saxena,S., Schmidt,J., Mellerowicz,E., Bako,L.S. and Bhalerao,R.P.

Differential stage specific regulation of cyclin dependent kinases during cambial dormancy in hybrid aspen

L Unpublished

2 (bases 1 to 1640)

3 Espinosa-Ruiz,A. and Bhalerao,R.P.

Direct Submission

L Submitted (17-MAY-2003) Department of Forest Genetics and Plant
Physiology, Swedish University of Agricultural Sciences (SLU), Umea
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PYELHDDNYULAMKECERPQSDGMAPNPPADGGEGSSMSSMYQPQILASPSTNTPVR
HPTSPPLEGI IKAAWKECERPQSDGMAPNPPADGGEGSSMSSMYQPQILASPSTNTPVR
                                                                                                                                                                                                      linear PLN 24-JUN-2003 (DP1) mRNA, complete cds.
                                                                                                                                                                                   227 HisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGly 246
                                                                                                      ValLysThrSerArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAla 226
                                                                                                                             843 GAACAACTGTACAGCTCAGGAAATGCTCCTAGTGGTGGTGTGTCGTTGCCTTTTATTCTG
                         188 GlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeu
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1. .1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 IleTyrSerGluLeuLysSerMetAlaHisIle--------GlyGlnGlyPhe 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 LysileLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLys 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 LyslysGluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLys 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GlyValHisIleLeuGluAlaSerSerValProProLeuProGlu 34
Submitted (31-AUG-1999) Department of Forest Genetics and Plant Physiology, SLU, Umea S-901 83, Sweden Location/Qualifiers
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    1640
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                                                                                                                                                       Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P., Ellero, C., Goff, S. and Glazebrook, J.

Burect Submission
Submitted (27-JAN-2003) Torrey Mesa Research Institute, Sy Research and Technology, 3115 Merryfield Row, San Diego, CUSA
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Oryza sativa (japonica cultivar-group) isolate 26539 DP TF mRNA,
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                     602
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                                                                                                                                                                                                                                                                                                                 399 GCCGCCCCTAATAAGAAGAAAAAGAGAGGTCAACGGGCTGTTGGAGCTGATAAG----- 452
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                                                                                                                                 --- GlyValHisIleLeuGluAlaSerSerValProProLeuProGlu 34
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                                                                                                                                                                                                                                                        AlaGlyGlyAsnAlaValGlnArgLysGly-----AlaValAspProAspLysAspArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 HisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGly
         AlaProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThr-----
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1 (Dases I to 1041)

2 (Dases I to 1041)

1 (Dases I to 1042)

2 (Dopor. B. Hutchison, D., Park, S., Guimil, S., Luginbuhl, P., Ellero, C., Goff, S.A. and Glazebrook, J.

Identification of rice (Oryza sativa) proteins linked to the
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ACCESSION VERSION

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AY224589 1140 bp mRNA linear PLN 05-FEB-2004 Oryza sativa (japonica cultivar-group) isolate 31182 E2F dimerization factor mRNA, complete cds.
                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.

1 (bases 1 to 1140)
Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P.,
Clooper, B., Autchison, D., Park, S., Guimil, S., Luginbuhl, P.,
Identification of rice (Oryza sativa) proteins linked to the
cyclin-mediated regulation of the cell cycle
Plant Mol. Biol. 53 (3), 273-279 (2003)
                                        TTTGCACTTCCAAATAACGATGGAACATCCCCTGATCAGCAACAGTATGATGAGAAAAAC 459
                                                                                                                                                                                                                                                          192 SerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeuValLysThrSer 210
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                                                                                                                                                                                                                                                                                                              GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191
                                                                                                                                                         132 GlulyslysglulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLyslleLysLys 151
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Cooper, B., Hutchison, D., Park, S., Guimil, S., Luginbuhl, P.,
Bllero, C., Goff, S. and Glazebrook, J.
Direct Submission
Submitted (27-JAN-2003) Torrey Mesa Research Institute, Syngenta Research and Technology, 3115 Merryfield Row, San Diego, CA 92121, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 CCTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1140
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Wipponbare"
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product==E2F dimerization factor"
protein_id="AAO72709.1"
/db_xref="GI:29371983"
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  LeuLysSerMetAlaHisIleGly
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AY224589.1 GI:29371982
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                                                                                                                                                                                                                                                                                                pSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSe 242
                                                                                                                                                                                                                                                                                                                                                                         Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
Nucleic acid molecules encoding plant cell cycle proteins and uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGlu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 GCGGCTGGTCCAGATAAGACTGGAAGAGGACTACGTCAATTTAGTATGAAAGTTTGTGAA 339
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                                                                                                                                     #98. GGATATTATATCTAAGGATAAAAGGAAATTCAGTGGAAGGGCTTGCCTCGG-----
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                                                                        -ACAAGTATGAGCGATGTTGAAGATTGAAGACAGAGATCATCGGACTGAAAGGTAGGAT
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                                                                                                                                                                                           eLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLe
                                                                                                                                                                                                                                                                      uProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAspAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysGluLys
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoj
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                             242 rileLeuGluGlyValArgArgAsnSerIleGlyArgAlaGlyArg 257
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/db xref="taxon:3702"
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CropDesign N.V. (BE)
Location/Qualifiers
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Sequence 33 from Patent WO0185946.
AX449314
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ASTSGGSAGSPESSRSEQHVPAAAGMAAGAAASTPISENTFLERINDLDIHGDDAPSSQ
APTSKKKKRGARAVGPDKGGRGLRQFSMKVCEKVESKGRTTYNEVADELVAEFADPNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgvalGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGlyAla 233
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                                                                                                                                                                                                                                                              ProProArgGlyGlyAlaAlaAlaAlaAlaAlaAlaLeuAspLeuThrGlyValHis
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111
43
77
63
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Nucleic acid molecules encoding plant cell cycle proteins and
                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Matches:
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CropDesign N.V. (BE)
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                               AX449342 1470m Patent W00185946.
AX449342.1 GI:21698089
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
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Ecker, J.R. (SSP/Salk)

and

(RIKEN GSC)

this work

1. .879 /organism="Arabidopsis thaliana"

/mol\_type="mRNA" /db\_xref="taxon:3702" /chromosome="5"

/clone="U60005"

contributed equally to this work as PIs Location/Qualifiers

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FEATURES
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Kim.C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carningi, P., Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kanja, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Ondera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Sakurai, T., Sakurai, Y., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 879)
Kim.C.J. (Chen.H., Cheuk.R., Shinn,P., Bowser,L., Carninci,P.,
Chan,M.M., Chang,C.H., Dale,J.M., Hayashizaki,Y., Hsuan,V.W.,
Ishida,J., Jones,T., Kantan,A., Karlin-Neumann,G., Kawai,J.,
Iam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Sarcu,M., Seki,M.,
Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K.,
Yu,G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and
Beker,J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-MAR-2003) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arbidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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GAACAAGTAATGAACATCATCGATACTCTCGGCTTATCTGCTTCCTGCCTTCAGAATCTG
                                                                                     184 LysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlylleArgLeu
                                                                                                                 860 ATACAGAGAAATGAGCACTTATATAGCTCAGGAAATGCTCCCAGTGGCGGTGTTGCTCTT
      ----LeuGlnAsnIle
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  LysGlnPheAspAsp-
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.879

CDS

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113
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                                                                                                                                                                ValGlnArgiyysGlyAlaValAspProAspLysApaDArgLysLysGluLysAlaAlaAla 59
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Mismatches:
Indels:
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          8.5e-26
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The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAS: Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to

Ecker, J.R.

113

516

212 969

DEFINITION

RESULT 14 ATH319027

8

ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                           134 LysGlulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGlu 153
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||| :::||| ||||||||||||| TCAAGAACTTCTGGAGGGCTTCGTCAATTGGAA 276
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337 ATTAAGCAAAAGGCAGAGAAGCCTTTGAATGAAAATGAGTACAATGAGAAGAAGAACATAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 AAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAAGTCAAG
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Nucleic acid molecules encoding plant cell cycle proteins and
therefor
                                                                                  AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer
                                                                                                                                                                                           MetalaHisIleGlyGln------GlyPheAspGluLysAsnIleArg
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Sequence 16 from Patent WO0185946.
AX449297.
AX449297.1 GI:21698044
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Direct Submission
Submitted (29-AUG-2001) Bergounioux C., UMR 8618, Chrs, IBP bat
Universite Paris-Sud, 91405 Orsay, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rossignol, P.
B2F family transcription factors: AtB2F-a and AtDP-a, induce Arabidopsis leaf cells to re-enter S phase
Uppublished
2 (bases 1 to 960)
Bergounioux, C.
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dp2a gene; E2F dimerisation partner protein.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Pred. No.:
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source

FEATURES

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gene

TITLE JOURNAL

AUTHORS

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Query Match:

.. No.:

ORIGIN

03-JUL-2002

PAT

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134 LysgluljeArgTrpMetGlyLeuSerAsnTyrArgTyrGluLys1leLysLysLeuGlu 153
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512 AGAGAAAAGGTCTCAAGTCTTGAGAGTCTTATGTCGAGAAATCAAGAGATGGTGAAG 571
                                                                                                                                                                                                                                                                                                                                                                194 AlaGluAsn --- ValAsnGlyIleArgLeuProPheValLeuValLysThrSerArgLys 212
                                                                                                                                                                                                                                                                                                                                                                                                              213 AlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGly 232
                                                                                                                                                                                                                                                                                                                                                                                                                           ||||::|||||||
92 GTGAGAAGGAAATTGATTGTTGATGATGATTCTGAAATTGGATCAGAGAAGAAAGGGCAA 151
                                                                                                     212 GCCAAGAAGATAACTACTTACAAGGAGGTTGCAGACGAAATTATTTTCAGATTTTGCCACA 271
                                                                                                                                                                                                                                                  392 AAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAAGTCAAG 451
                                                                                                                                                                                                                                                                                                                                                                               80 AlaLysGlyArgThTThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer 99
40 ValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAlaAla 59
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AAX76730 ACN88986

AAT10582 AAS96410

4BL08071

ABV26838 ABV20992

ACN38014

**ABL65866** 

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E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of a wheat E2F-dimerisation partner (DP) protein.
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/product= "B2F-dimerisation partner (DP) protein"
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11-NOV-1999;
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-Q=/cgn2_1/USPTO spool/US10088830/runat_04022005_122602_29549/app_query.fasta_1.455
-DEA Genseq=G_16Dec04 -QFWT=fastap -SUFFIX=D11.xng -MINMATCH=0.1 -LOOPCL=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                    nucleic search, using frame_plus_p2n model
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Aah33503 Human col Aag65344 Transcrip Aar65325 Cotton cD Ad063216 Transcrip Aa894979 Human DNA Ad062851 Transcrip

ADM78581 ADP13337 ADR25496 AD019868

AAD59591 ADK67024 ADI32073

ALIGNMENTS

ADO63216 AAS94979 ADO62851

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The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds.
                               560 CAAAACATCAAGTTACGTAACCAAAACACTGGAAAGCTCAGCAGAGAATGTTAATGGCATC
                                                                                                                                                          620 CGCCTTCCATTCGTATTGGTCAAGACATCTAGGAAAGCAAGGGTGGAAATTGAGATTTCA
                                                                                                                                                                                                                   AspAspSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAsp
                                                                                                                                                                                                                                                                                                                                241 LeuSerIleLeuGluGlyValArgArgAsnSerIleGlyArgAlaGlyArgAlaThrLeu
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GlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsnGlyIle
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                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue so to alter plant cell, organ or tissue
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for e.g. altering cell proliferation characteristic such as to alter
plant cell, organ or tissue size.
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                                                                       ATGCCCTCCCTCCCGCGCGATGCCGCGCGCGCGCTCCGCCGCCGCCCGGCCAAC
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                                                         MetAlaProProArgGlyGlyAlaAlaAlaAlaAlaAlaLeuAspLeuThrGly
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Plant; transcription factor; transgenic plant; abiotic stress tolerance; sembtic stress tolerance; sombtic stress tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds. Transcription factor G2981 coding sequence, SEQ ID 1549. (MEND-) MENDEL BIOTECHNOLOGY INC. 17-DEC-2002; 2002US-0434166P. 24-APR-2003; 2003US-0465809P. 18-SEP-2003; 2003WO-US030292 18-SEP-2002; 2002US-0411837P Arabidopsis thaliana WO2004031349-A2. 15-APR-2004

New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.

Reuber TL;

Adam LJ, R Sherman BK;

Creelman RA, , Keddie JS,

Ratcliffe O, C: V, Dubell AN,

Jiang C, Heard JE, Riechmann JL, Haake

WPI; 2004-330163/30. P-PSDB; ADO63083.

Claim 1; SEQ ID NO 1549; 510pp; English.

decreased anthocyanin levels. Note: The sequence data for this patent did The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed brotein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and not form part of the printed specification, but was obtained in ftp.wipo.int/pub/published\_pct\_sequences. format directly from WIPO at

Sequence 1158 BP; 374 A; 261 C; 253 G; 270 T; 0 U; 0 Other;

ADO63082 standard; DNA; 1158

(first entry)

15-JUL-2004

ADO63082

15-APR-2004

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                                                                                                                                           37 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys 56
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|TAAAGAACGAACTCTCACTTAGGAACAGAATTGAGAAGAAAACTGCATATTCCCAA
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Mismatches:
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Matches:
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tungal disease and particularly Erysphe, Fusarium and Botrytis, chugal disease and particularly Erysphe, Fusarium and Botrytis, concreased tolerance to multiple fungal pathogens, increased resistance to increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ABA, concreased sensitivity to ABA, reduced sensitivity to ABA, and a sensing, increased tolerance to sugars, altered furbour structure, loss of flower increased tolerance of fertility, altered furbone meristem development, altered branching pattern, altered trichome density, altered branching pattern, altered trichome development, altered branching pattern, altered trichome structure, altered richome development, altered shade avoidance, altered seed development, altered shade avoidance, altered seed development, altered shade development, altered shade concreased altered seed coloration, altered cell proliferation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell catch, lethality when overexpressed, altered necrosis patterns, increased coll proliferation, altered seed solarity, altered seed coloration, altered seed shape, large seedlings, dwarfed plants, dark green or gray leaves, also grown altered seed solarity, altered seed coloration, altered seed shape, large content, altered seed coloration, altered seed shape, large content, altered seed bazial/daxial polarity, altered seed coloration, altered seed shape, large content, altered seed brings and content, altered seed shape, large content, altered seed shape, large seed increased anthocyanin levels, and content, altered seed coloration, altered seed seed coloration, altered seed shape, large content, altered seed shape, large content, altered seed coloration seed seed coloration of the printed seed seed coloration seed seed coloration of the property altered seed coloration seed seed coloration increased anthocyanin levels,
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                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Sherman BK;
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Keddie JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 609; 510pp; English.
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Riechmann JL, Haake V, Dubell AN,
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17-DEC-2002; 2002US-0434166P.
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GlyasnalavalGlnargLysGlyalavalAspProAspLysAspArgLysLysGluLys 56

Gaps:

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                                                                                                  97 LeuLysSerMetAlaHisIleGly-------GlnGlyPheAspGluLysAsn 111
                                                                                                                                                                                                                LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
                                                                                                                                                                                                                                                     GlulleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191
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                                                                                                                                                                             GluiysiysgluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLys 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                        SerSerAlaGluAsnValAsn--GlyIleArgLeuProPheValLeuValLysThrSer
|||||||
AGCTCAGGAAATGCTCCCCAGTGGCGGTGTTGCTTTTTATCCTTGTCCAGACTCGT
                                                                LysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGlu
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GAACTGGAAGAACAATATGTAGGCCTTCAGAATCTGATACAGAGAAATGAGAGCACTTATAT
                                                                                                                                                                                                                                                                                                                              211 ArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe
                                                                                                                                                                                                                                    Traaagaacgaacgactctcactraggaacagaartgagaagaaagaaacrgcaratrcccaa
                                                                                                                                                                                                                                                                                                                                        760 CCTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC
                            AlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGlu
                                                                                                                                                                                                                                                                                                                                                                   AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 25934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0121825P.
99US-0123180P.
99US-0125548P.
99US-0126264P.
99US-0126785P.
99US-0126785P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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99US-0144334P

99US-0144334P

99US-0144332P

99US-0144834P

99US-0144834P

99US-0145088P

99US-0145088P

99US-0145089P

99US-0145138P

99US-0145218P

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99US-0154779P.
99US-0155139P.
99US-0155486P.
99US-0156458P.
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99US-0157753P.
99US-015786SP.
19-70L-1999;
19-70L-1999;
20-70L-1999;
20-70L-1999;
20-70L-1999;
21-70L-1999;
21-70L-1999;
22-70L-1999;
22-70L-1999;
22-70L-1999;
23-70L-1999;
                                                                                                                                                                                                                                                                                                                                             25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                             04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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	Length: 1618 Matches: 104 Conservative: 40 Mismatches: 68 Indels: 6 Gaps: 2	2 (1-261) x AAC39795 (1-1618) GlyAsnalaValGlnArgLysGlyAlaValAspProAspLysAspArgLysBLysGluLys 56 :::
99US-0159235P. 99US-0159329P. 99US-0159330P. 99US-0159331P. 99US-015963P. 99US-015963P. 99US-0160741P. 99US-0160761P. 99US-016098P. 99US-016098P. 99US-016098P. 99US-016098P. 99US-016098P. 99US-016098P. 99US-016135P. 99US-016135P. 99US-016135P. 99US-016135P. 99US-016135P. 99US-016135P.	1.92e-39 492.00 7: 66.06 77.71 37.30 3	2 (1-261) x AAC39795 (1-1618) GlyAsnalaValGlnArgLysGlyAlaVa    :::
13-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 18-OCT-1999 21-OCT-1999 21-OCT-1999 21-OCT-1999 22-OCT-1999 22-OCT-1999 22-OCT-1999 25-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999	lignment Scores: red. No.: Score: Sercent Similarity Aset Local Similar Phery Match:	10-088-830-2 37 G1 468 G6 468 G6 57 A1 528 AA 588 AA 112 I1 112 I1 152 I16 828 I17 828 I17 172 G1 192 Se
**************************************	Ali Pre Sco Sco Per Per Oue	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$

death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed protein content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

8  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9  $\times$  9

Other;

U; S

0 .. H

Sequence 1443 BP; 419 A; 273 C; 343 G; 403

Similarity:

Best Local

Percent Similarity:

Alignment Scores:

Pred. No.:

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The present invention relates to novel plant transcription factor

proteins (I) and nucleotide sequences (II) (Ab061534-Ab063778). The

sequences can be used to produce transgenic plants, which overexpress

(II), where the transgenic plant has an altered trait as compared to a

contransgenic plant or wild-type plant. The transgenic plant comprises

con altered trait selected from increased tolerance to abiotic stress,

increased germination in cold, increased tolerance to heat, increased

confirmation in heat, increased tolerance to heat, increased

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation in heat, increased tolerance to disease, including

confirmation, altered sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ABC, altered sugar sensing, early flower determinacy

confirmation, altered sensitivity to ABA, reduced sensitivity altered sensitivity altered vascular tissue structure, reduced

confirmation, altered seed development, altered branching pattern,

altered trichome structure, altered vascular tissue structure, altered vascular tissue structure, altered vascular tissue structure, altered vascular tissue structure, altered seed development, altered seed development, altered seed development, altered seed development, altered seed development, altered seed development, altered seed development, altered seed development, altered seed development, altered seed development, alte
                       CTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; transcription factor; transgenic plant; abiotic stress tolerance; sometic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
211 ArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reuber TL;
                                                                                                                            231 AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor G2981/2982 orthologous sequence, SEQ ID 1319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adam LJ, R
Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratcliffe O, Creelman RA, V, Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1319; 510pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                 ВЪ
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                                                                                                                               ADO62852 standard; DNA; 1443
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                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Riechmann JL, Haake
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 GluLysijeLysLysLeuGluGluValArgLysGluLeuValAsnLysijeArgAsnLys 166
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                                                                                                                                                                                                                                                                                GlulleTyrSerGluLeuLysSerMetAlaHisIle------GlyGlnGly 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyr 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 LysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArg 186
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                                                                                                                                                                     168 AACÁGCTTGCCACCTCGGTCGATAAACTATTCTCAAATTGAACCATCTCGACGTACAT 227
                                                                                                                                                                                                                               ----TCTCTTGCTGGCAAGAAAAAG 275
                                                                                                                                                                                                                                                               71
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                                                                                                                                                                                                                                                                                                                                          336 ATGAAAGTGTGAGAAAGGTAGAAAGCAGGGAAGAAGAACCACATACAATGAGGTGGCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576 AATGATTGAAGAACTAAAGACAGAGCGGCTTGGGCTCAGGAATAGAATTGAAAAGAAA
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                                                                                                                                                                                                   32 LeuProGlualaGlyGlyAsnalaValGlnArgLysGlyAlaValAspProAspLysAsp
                                                                                                                                                                                                                                                               ArgLysLysGluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSer
                                                                                                                                                                                                                                                                                                                       72 LysllevalCysGluLysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 AsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeuProPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        696 AATGAGCAGTTATAAGCTCAGGAAATCCTCCCAGTGGAGGTGTATCTTTACCCTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     756 TTGGTACAGACACGTCCTCATGCAACTGTGGAAGTGGGAAATATCAGAAGATATGCAGCTT
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   1443
106
42
70
25
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                             Gaps:
                                                                                                         US-10-088-830-2 (1-261) x ADO62852 (1-1443)
                                                                                                                                                                                                                      228 GCTGATGATGCTGGATCACACGCT-
1.48e-38
482.50
60.91%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel plant transcription factor proteins (1) and mucleotide sequences (11) (AD061534-AD065778). The sequences can be used to produce transgenic plants, which overexpress (CI), where the transgenic plant has an altered trait as compared to a non-transgenic plant for wild-type plant. The transgenic plant comprises constructed from increased tolerance to abidic stress, increased tolerance to cold, increased tolerance to heat, increased colerance to conditions, increased tolerance to heat, increased colerance to low introgen conditions, increased tolerance to disease, increased tolerance to cold, increased tolerance to disease, increased tolerance to cold increased tolerance to low mitrogen conditions, increased tolerance to whosphate conditions, increased tolerance to disease, including thugal disease and particularly Erysiphe, Fusarium and Botrytis, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, colorance to sugars, altered carbon/nitrogen sensing, early flowering, latered track flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered steem morphology, altered vascular tissue structure, reduced colorance, altered seed development, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll development, altered phase change altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, altered coll proliferation, 
                                                                                                                                                                                                                                                                  Plant; transcription factor; transgenic plant; abiotic stress tolerance; semotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Sherman BK;
                                                                                                                                                                                                                                Transcription factor G2981/2982 orthologous sequence,
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V, Dubell A
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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  246 GlyValArg
                                    876 GCAATGAAA
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Riechmann JL,
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altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedpromyl content, altered leaf premyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent on tof form part of the printed specification, but was obtained in the electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AlaGlyGlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLys
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|TIGTATGGCTCAGGCAATGCTCCTAGTGGTGGTGTTAACGGTTTATTTTAGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 SerGluLeuLysSerMetAlaHisIleGlyGlnGly-------PheAspGlu
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                                                                                                                                                            Sequence 1153 BP; 337 A; 225 C; 267 G; 324 T; 0 U; 0 Other;
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114
40
82
31
6
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Matches:
Conservative:
Mismatches:
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476.50
57.68%
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36.13%
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yTrpGlyLeuArgGluTyrSerLysIleValCysGl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, sensecence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body
                                                                                                                                                               cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds.
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding a cell proliferation-related by Dypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and producing enhanced food crops.
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                                                                                                                                         Cell proliferation-related nucleic acid sequence #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ArganSerIleGlyArgAla 255
                       ---AATTTTTGCGGAAGATCA 803
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471.50
57.61%
41.30%
35.75%
                                                                                                                 (first entry)
                                                                     DNA;
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                                                                     standard;
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Best Local Similarity:
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126 uArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTy 146
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                                                         GTTTGCAGACCCCAACAATAATTTTGCATCACCTGATCCTGACAACACCAAACACACAA 437
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                                                                                                                                                                                                                                                                                              146 rGluLyslleLysLysLysLeuGluGluValArgLysGluLeuVal-----AsnLysil 163
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                                                                                                                                                                                     609 CGACAAGAAAATGCATATTTGCAGGAGTTAGAAGATCAATTTGTAGGTCTTCAAAACTT
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AlaProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThrGlyVal

x ADQ36844 (1-1041)

US-10-088-830-2 (1-261)

Query Match DB:

21

42 ArglysGlyAlaVal-AspProAspLysAspArglysLysGluLysAlaAlaAlaProAr

P-PSDB; AAU72514. 

New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

Claim 38; Page 185-186; 316pp; English.

The invention relates to a novel cell cycle protein (CCP) and the polympotic and which binds to the which modulates the activity of the polympotide and which binds to the polympotide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Abaldopsis thalians, rice, wheat, cycle or growth of a plant such as Abaldopsis thalians, rice, wheat, cycle or growth of a plant such as Abaldopsis thalians, rice, wheat, compared to a plant such a research cand canola. CC maize, tomato, alfalfa, oilseed rape, soybean, sumflower and canola. CC conclet cacid and polypeptide molecules are useful as modulating agents in plants. CCP is useful to treat a trivity. Compounds that bind to or modulate the activity of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polymucleotide is useful for modifying cell fate, plant development, polympotides are useful as herbicides or plant growth regulators. The polymucleotide is useful for modifying cell fate, plant development, in coll cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, plant morphology, biochemistry and/or physiology, the length of the coll cycle of and the anti-CCP antibone, where the protein involved in the cell cycle due to and the anti-CCP antibons, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, continion, heat, drought, salt stress, or biotic stress such as cold, activity of a part of the protein involved in the cell cycle detect plant architecture, plant quality traits, plant reproduction and seed development, endocreduplication in storage cells, storage crissons and/or generate antibodies. CCP protein is useful so an immunogen to generate antibodies. CCP protein is useful feels on modulate collection or modulate is useful set and to m nvention

BP; 366 A; 256 C; 247 G; 262 T; 0 U; 0 Other; Sequence 1131

Length: Matches: Conservative: Mismatches: [ndel8: Gaps: .36e-37 466.50 63.76% 46.33% 35.37% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local

399 220 GGTGATGATGCTGGTTCTCAGGAGCTTCTGGTGTAAGAAGAAGAAGAAGAGGGGACAGCGT 279 -----GinGlyPheAspGluLysAsn 111 400 TTTGCACTTCCAAATAACGATGGAACATCCCCTGATCAGCAACAGTATGATGAGAAAAAC 459 IleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys 131 AlaAlaAlaProArgileThrGlyTrpGlyLeuArgGluTyrSerLysIleValCysGlu 76 GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysGluLys 56 LysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGlu 96 AAGGTGGAAAGCAAAGGAAGGACAACTTACAATGAGGTTGCAGACGAGGTTGTTGTTGCTGAA 97 LeuLysSerMetAlaHisIleGly-----US-10-088-830-2 (1-261) x AAS96304 (1-1131) 57 280 77 340 112 셤 g 셤 원 ò ò ઠે ઠે ò

639 672 732 230 733 CCTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC 792 LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171 GlulyslysgluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysileLysLys 151 GluileGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191 SerSerAlaGluAsnValAsn---GlyIleArgLeuProPheValLeuValLysThrSer 211 ArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe 248 231 AsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 640 GAACTGGAAGAACAA-----192 172 152 ద 임 Š 셤 ò g ò g ò 셤 ò

ADQ36854

ADQ36854 standard; DNA; 1140

BP

AD036854;

(first entry) 07-OCT-2004 Cell proliferation-related nucleic acid sequence #7.

cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response; ds. 

Oryza sativa.

WO2004061122-A2

22-JUL-2004

23-DEC-2003; 2003WO-US041200.

26-DEC-2002; 2002US-0436565P.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Cooper B;

WPI; 2004-534388/51.

New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops.

Claim 3; SEQ ID NO 13; 408pp; English.

The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for acid modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related nucleic acid sequence. The present sequence is published separately from the main body of the specification as EPO data.

Sequence 1140 BP; 327 A; 268 C; 310 G; 235 T; 0 U; 0 Other;

Alignment Scores:

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AlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLysBlysGluIleArgTrp 138
                                                                                                                                                                     MetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGluGluValArgLysGlu 158
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Plant; transcription factor; transgenic plant; abiotic stress tolerance; sendiction factor; and tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                       New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                Transcription factor G2981 orthologous sequence, SEQ ID 1830.
                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1830; 510pp; English.
                                                                                                                                                                                                             d JE, Ratcliffe O,
Haake V, Dubell A
                                                                                                                                                                                              (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                    17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                            18-SEP-2003; 2003WO-US030292
                                                                                                                                                             18-SEP-2002; 2002US-0411837P.
                (first entry)
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                                                                                                           WO2004031349-A2.
                                                                                                                                                                                                              Jiang C, Hear
Riechmann JL,
                15-JUL-2004
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                                                                                          Zea mays.
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Reuber TL;

Adam LJ, R

Creelman RA, Keddie JS,

Dubell AN,

The present invention relates to novel plant transcription factor

CC proteins (1) and nucleotide sequences (11) (ADO6154-ADO63778). The

sequences can be used to produce transgenic plants, which overexpress

(11), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises

(11), where the transgenic plant has an altered trait as compared to an altered trait selected from increased tolerance to abortic stress, increased tolerance to cold, increased tolerance to cold; increased tolerance to conditions, increased tolerance to freezing conditions, increased tolerance to disease, including to phosphate conditions, increased tolerance to disease, including to increased tolerance to multiple fungal pathogens, increased tolerance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABC, altered sugar sensing, increased tolerance to sugars, increased tolerance to sugars, altered sensitivity to ABC, altered sugar sensing, increased tolerance to sugars, altered subor, mittogen sensing, early flowering, latered subor, altered subor, altered wascular tissue sensing, altered subor, altered subor, altered wascular tissue structure, altered subor, altered vacular tissue structure, altered density, altered trichome structure, altered vacular tissue structure, altered seed development, altered bands and altered cell proliferation, altered cell expension, altered cell proliferation, altered cell expension, altered density, altered cell proliferation, altered density, altered cell proliferation, altered seed intered seed sensectence, abnormal embryo altered seed richome structure, altered development, altered cell proliferation, altered seed sensition, altered seed sensectence, abnormal embryo altered seed prolaming, altered seed sensected cell proliferation, altered seed sensition, altered seed sensected and seed coloration, altered seed seed selection content, altered seed seed coloration, altered seed seed o electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

ADO63363 standard; DNA; 1245 BP

RESULT 11 ADO63363 ID ADO6 XX

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The present sequence encodes a corn DP (not defined) polypeptide. The polypeptide is a transcription factor that activates transcription of numerous genes involved in DNA replication, thus playing a role in the G1 to 8 transition in the cell cycle. Do, also called Driff (differentiation regulated transcription factor 1) has been shown to form specific multiprotein complexes with the retinoblastoma susceptibility protein, plo7, cyclins and cdk2. The DP polynuclectide was used to produce a transgenic plant. The DP nucleic and proteins are useful for increasing transformation efficiency in plants by increasing the number of dividing cells in the plant (dividing cells may be more receptive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
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                                                                                                                                                                             DP polypeptide; transcription factor; gene transcription; cell cycle; DNA replication; DRTF; differentiation-regulated transcription factor 1; transgenic plant; transformation efficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plants comprising an expression cassette consisting of a DP nucleic acid, when expressed, the nucleic acid increases the efficiency of plant cell transformation by increasing the number of dividing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAspLeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 900 BP; 293 A; 178 C; 231 G; 195 T; 0 U; 3 Other;
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                                                                                                                                       DNA encoding a transcription factor designated DP
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                     polypeptide"
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                                                                                                                                                                                                                                                                                                                         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 70-71; 76pp; English.
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AAA59702 standard; DNA; 900
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                                                                                           (first entry)
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P-PSDB; AAB07975.
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                                                AAA59702;
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New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

Claim 38; Fig 39; 316pp; English.

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Magyar

Acosta JAT,

Veylder L,

De

P-PSDB; AAU72542

12-MAY-2000; 2000US-0204045P

CROPDESIGN NV. Boudolf V,

(CROP-) Inze D,

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124 IleAlaLeuArgValIleAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsn 143
                                                                                                                                 104 GlyGlnGlyPheAspGluLysAsnileArgArgArgValTyrAspAlaPheAsnValLeu 123
                                                                                                                                              274 GCGCAACAATATGATGAGAAAAATATACGACGAAGAGTTTATGATGCTTTGAATGTTCTG 333
                                                                                                                                                                                                                                                                                                     219
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                CCTACGAGCAAGAAGAAAAGGAGAGGCACACGGGCAGTGGGTCCTGATAAAGGTAACCGG 129
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-------GGACTGCGCCAGTTTAGTATGAAA 153
                                                                                                 214 GTTGCTGAGTTTACAGACCCCAACAATAATATTGAGGCACCAGATCCTGATAACCCTAAC 273
                                                                                                                                                                            161 AsnlysileArgAsnlyslysAlaLeuLeuGinGluIleGluLysGinPheAspAspLeu 180
                                                                                                                                                                                                                                              GlnAsnIleLysLeuArgAsn---GinThrLeuGluSerSerAlaGluAsnValAsnGly 199
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| Caaaacctgattcaacgaaatgaacagtcatatggttcagaaacacgccttctggtgga 564
                                                                                                                                                                                                                                                                                                               SerAspAspSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAsp 239
                                                                                                                                                                                                                                                                                                                                                       684
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                                                                                                                                                                                                                                                                                                                                                36 GlyGlyAsnAlaValGlnArgLysGly-----AlaValAspProAspLysAspArgLys
                                 54 LysGluLysAlaAlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLysIle
                                                                                  GTTTGTGAGAAAGTTGAAAGTAAAGGGAGAACAACATATAATGAGGTGGCAGATGAACTT
                                                                                                                                                                                                                                                                                                     200 IleArgLeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIle
                                                                                                                                                                                                    144 TyrArgTyrGluLysIleLysLysLeuGluGluValArgLysGluLeuVal
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                                                                                                                                                                                 Cell cycle protein, CCP, ss; cell cycle regulation, herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield.
                                                                                                                                              Arabidopsis cDNA encoding cell cycle protein CCP33.
                                                                                                                                                                                                                                                                                                                                                                           14-MAY-2001; 2001WO-IB001307
                                                                                                           (first entry)
                                                                                                                                                                                                                                                              Arabidopsis thaliana
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WO200185946-A2.

15-NOV-2001

26-FEB-2002

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The invention relates to a novel cell cycle protein (CCP) and the polymucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the collypeptide and which binds to the polypeptide and which binds to the collypeptide and an anti-CCP antibody is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, aliase, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polymucleotide is useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physiology, the length of the Cl, c, G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, csed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, nodule function, dwarfism in plants, sender and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle deprivation, heat, drought, salt stress, cor biotic stress such as cold, nutrient convirtuned are minimucled to medulate e.g. enhance crop yields, and attenuate convirtunely plant quality traits, plant reproadcution and seed cells to path and and plants or its parts. CCP is useful as an immunogen concerned antibodies. CCP protein is useful as an immunogen or convirture of protein is useful as useful as an immunogen proper protein plant grants. The polymunication is useful as useful as an im
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   occurring CCP substrates. The polynucleotide is useful for expressi protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and modulate CCP activity. The present sequence encodes a CCP protein o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1442 BP; 451 A; 321 C; 297 G; 373 T; 0 U; 0 Other;
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                                                ArgvalTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLysLys 134
                                                                       155 ValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIleGlu 174
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800 GAACAAGTAATGAACATCATCGATACTCTCGGCTTATCTGCTTCCTGCCTTCAGAATCTG 859
                                                                                                                                                                               184 LysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeu 202
                                                                                                                                                                                              919
                                                                                                                                                                                                                                       SerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSer 242
                                                                                            GluileArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysileLysLysLeuGluGlu 154
       AlalysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer 99
                                                                                                                                                                                                                                                                                                                                                                      corn; maize; cell cycle regulatory protein; transcription factor;
                                                                                                                                                                                        ProPheValleuValLysThrSerArgLysAlaArgValGluIleGluIleSerAspAsp
                                    GlnGlyPheAspGl
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                                    100 MetAlaHisIleGly---
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                                                                                                                                                                                                                                                                                                                                                        Corn DP-2 cDNA clone.
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                                                                                                                                                                                                                                                                                                                                                                       DP-2; corn;
herbicide;
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This is the nucleotide sequence of a contig assembled from the CDNA inserts in clones p0005.Cbmfh2zr, cdelc.pk001.j13 and cen3n.pk0183.bi. It encodes a portion (see AAY32164) of a corn protein that shows homology to human cell cycle regulatory protein DP-2. The deduced amino acid sequence of this cDNA represents 50% of the middle region of the DP-2 protein. The coff constructed from cDNA libraries constructed from corn constructed from corn construction. The invention relates to nucleic acid fragments (see AAZ34575-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory protein, see AAZ3159-67). It also relates to the cell cycle regulatory protein, in sense or antisense orientation, where construction of a chimeric gene encoding all or a portion of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein, in sense or antisense orientation, where cycle regulatory protein in a transformed host cell. The nucleic cycle regulation in plants, provide genetic tools to enhance cell growth in cycle regulation in plants, provide genetic tools to enhance cell growth in the proteins may be used to facilitate studies of call cycle more stable cransformations. The proteins may also provide targets to facilitate constructions that may a be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||| ::|||||||:::::--ACTAGTATAAGGTGATATGAGATTGAAGACTGAGCTTGTGGGACTGAAA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 CCTACGAGCAAGAAAAAGCAGAGACACACGGGCAGTGGGTCCTGATAAAGGTAACCGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 GTTTGTGAGAAAGTTGAAAGTAAAGGGAGAACAACATATAATGAGGTGGCAGATGAACTT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 LysGluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIle 73
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:::||| GTTGCTGAGTTTACAGACCCCAACANTAATATTGAGGCACCAGATCCTGATAACCCTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1193 BP; 365 A; 220 C; 305 G; 302 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                           Plant-derived cell cycle regulatory proteins.
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                                                                                                                       Claim 12; Page 41; 44pp; English
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P-PSDB; AAY32164
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plant morphology, biochemistry and/or physiology, the length of the G1, S G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, nodule function, dwarfism in plants, senescence, tolerance or resistence to stress. CCP, the polymucleotide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, mutrient deprivation, heat, drought, salt stress, or biotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as carefuled development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polymuclesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the

Seguence 1114 BP; 378 A; 197 C; 243 G; 296 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels:

2.77e-33 428.50 64.32% 41.31% 32.49%

Similarity:

Query Match: Best Local

Percent Similarity:

Alignment Scores:

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                                                                                                                                                                                                                                                                                                                             683
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                                                                                                                                                                                     GTGGCTTTGCCATTCATCCTAGTCCAGACCCAACCTAGCTACCGAGAAGTTGAGATA
                                                                                                                                                                                                                                                                                                   GGTAGAATTGAGAAAAAGTGTTTACTTACAGGAGCTACAAGATCAATATGTAGGTTTG
                                                                                          11eArgLeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIle
                                                                                                                                                                                                                                                                 SerAspAspSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAsp
                                                                                                                                                                                                                                                                                                                                                                                  -----Arg
                                                  GlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---Gly
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134 LysGlulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLeuGlu 153 92 Greagaaggaaarrearerreareargarrergaarregarregareagagaaaggeeaa 151 114 ArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLys 133 392 AAGGAAATCCGGTGGAAAGGACTTCCTATTACCTGCAAAAAGGATGTGGAAGAAGTCAAG 451 -----GlyPheAspGluLysAsnIleArg 332 CGGAGAGTCTACGATGCGCTCAATGTGTTCATGGCGTTGGATATTATTGCAAGGGATAAA 154 GluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIle 60 ProArglleThrGlyTrpGlyLeuArgGluTyrSerLyslleValCysGluLysValGlu 80 AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer 212 GCCAAGAAGATAACTACTACAAGGAGGTTGCAGAAGGAAATTATTTTTGCCACA 174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 194 AlaGluAsn---ValAsnGlyIleArgLeuProPheValLeuValLysThrSerArgLys 213 AlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGly 1114 88 49 69 7 Gaps: US-10-088-830-2 (1-261) x AAS96287 (1-1114) 100 MetAlaHiBIleGlyGln----ò 셤 쉽 ò 셤 8 g 임 임 셤 셤 ò ઠે ઠ ઠે 8 8 g ઠે The invention relates to a novel cell cycle protein (CCP) and the polymucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and which binds to the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful for modifying cell fate, plant development, New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

211

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79

113 331

271

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173

Claim 38; Fig 16; 316pp; English.

WPI; 2002-062249/08. P-PSDB; AAU72497 셤

233 AlaProPheThrLeuHisAspAspLeuSerIleLeuGlu 245

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Search completed: February 6, 2005, 22:04:22 Job time : 588 secs

Zea mays GR Eb019 CR286882 EST724739

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Homo sapi ALS47857

NXSI 116 AL965517

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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryze,

I (bases 1 to 1119)

S Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,

Jiao,Y., Sun,N., Zhao,H., Yuan,L.,

Mong,G.K.S., Deng,X.W. and Wang,J.

An analygis of transcriptional regulation of the rice genome and

its comparison to Arabidopsis

Unpublished (2004)

Contact. Chen

Department of Bioinformatic

Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80488576

Email: Chenchengenomics.org.cn
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CL959517.
CL959517.1 GI:52373702
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/mol_type="genomic DNA"
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-WODEL=frame+_p2n.model -DEV=xlh
-Q=/Gqn2_I/USPTO_spool/US1008830/runat_04022005_122603_29569/app_query.fasta_1.455
-DB=SST _QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START=1 -END=-1 -WAYRIX=blooum62 -TRANS=human40.cdi -LiST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM==EXT -HEAPSIZE==500 -MINLENE = 0 -MAXENE=200000000
-USER=USI008830 @CGN 1 1 3437 @runat 04022005_122603_29569 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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(c) 1993 - 2005 Compugen Ltd.
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/db_xref="taxon:39946" /clone lib="Oryza sativa Express Library" /note="Oryza sativa exon trapped genomic sequences " Alignment Scores:	-10-088-830-2 (1-261) x CL959517 (1-1119)  1 MetAlaProProArgGlyGlyAlaAlaAlaAlaAlaThrAlaAlaLeuAspLeuThrGly	DD 1 ATGGCGCCTCCCTGCGGCGGTGGCGGCGGCTGCCTCCGCCCGGCCCTGGCCAAC 60 Qy 21 ValHislleLeuGluAlaSerSerValProProLeuProGlu	Qy         34	43 Ly8GlyalavalaspProAspLysAspArgLysGluLysAlaAlaAlaAlaPro ii:	Oy 61 ArgileThrGlyTrpGlyLeuArgGluTyrSerLysile73 	352 CCAGGGTTATCGCGCCCCGGCGGTAAACACTGTTACCGCGGGAGGTTACCGCGGTATT	Db         412 ACATTACCGTACCCGGCGGTAAGCCTGGTAACCGCGGGGTTACCGGCGGT 471           Qy         74	Qy         85 ThrTyrAsnGlu	89ValAlaAspGluIleTyrSerGluLeuLysSerMetAlaHisIleGlyGlnGly	Db 652 TTTGATGAGAAGAATATTAGGCGGAGGGTATATGATGCTTTCAATGTGCTCATTGCAATT 711  Qy 127 ArgVallleAlaLysGluLysLysGlulleArgTrpMetGlyLeuSerAsnTyrArgTyr 146  Db 712 CGTGTTATTGCAAAAGATAAAAGGAGATAAAGTGGATGGCCCTTACTAATTATAGATAC 771	Qy     147 GluLysIleLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLys 166       Db     772 GAAAAGATACAGAAGTTGGAGGAAGTTCACAAAAAACTCATCACCAGGATCAAGAATAAG 831       Qy     167 LysAlaLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArg 186

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Cryza sativa (indica cultivar-group)

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Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

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Entractophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Brankiewich, Stress; Oryza.

I (bases 1 to 765)

Ss Bennett, J., Arunugam, K., Lafitte, R., Wen, J., Rudd, S. and

Bruskiewich, R.M.

IRRI Drought Stress Panicle CDNA Library

U Unpublished (2002)

On Dec 2, 2002 this sequence version replaced gi:25994251.

Contact: Richard Bruskiewich

Blometrics and Bioinformatics Unit

International Rice Research Institute

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Tel: +63-2-845-0563
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AF53-Rpf 05 M03 T7 008.abl IRRI Drought Stress Panicle Library oryza sativa (indica cultivar-group) cDNA clone C0001827 5' similar to Transcription factor DP-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1), mRNA sequence.
CA764996.2 GI:27546711

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international Rice information System (IRIS;
http://www.iris.irri.org): D0201826
Assignment of putative function to the sequence by S. Rudd of the
                                   90 AlaAspGluIleTyrSerGluLeuLysSerMetAlaHisIleGlyGlnGlyPheAspGlu
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Unpublished (2003)
Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
SOU# Cao Bao Road, Shanghai 200233, China
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cona est clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR289243 Oryza sativa library (Han B) Oryza sativa cDNA clone p704a10p5, mRNA sequence.
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                                                                                                                                                                                                                                                                          ArglysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPhe 230
                                                                                                                                                                                                                                                                                                                                                AsnGlyAlaProPheThrLeutisAspAspLeuSerIleLeuGluGlyValArgArgAsn 250
                                                                                                                            GlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeu 190
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                                                      LysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeu
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/clone="p704a10p5"
/clone_lib="Oryza sativa library (Han B)"
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Matches:
Conservative:
Mismatches:
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Location/Qualifiers
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CR289243
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BE456002.3 GI:16318905
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                                                                                                                                            /db_xref="texon:39946"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVSWEG0019D17f Hordeum vulgare pre-anthesis spike EST 22-OCT-2001 HVSWEG0019D17f Hordeum vulgare pre-anthesis spike EST library HVSDMA0008 (white to yellow anther) Hordeum vulgare subsp. vulgare EDNA clone HVSWEG0019D17f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 GCAGAAAGTGTTAATGGCATCCTCCTTCCGTTCTTATTGATCAAGACATCCCGAAAAGCA 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 ArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPheAsnGlyAla 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 AGGGTGGAAATTGAGATTTCGGAAGATTCAAAGTTTGCACGGTTCGACTTCAACGGTGCA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 TyrSerGluLeuLysSerMetAlaHisIleGlyGlnGlyPheAspGluLysAsnIleArg 113
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Munich Information Center for Protein Sequences
                                                                                                                                                                                                                                                                                                                                                                                               765
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Conservative:
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/lone lib="Hordeum vulgare pre-anthesis spike EST library //lone lib="Hordeum vulgare pre-anthesis spike EST library HVcDNAÖ008 (white to yellow anther)"
//note="Vector: lambdaZAPP: Site= 1: ECOR1; Site 2: XhO1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spike with awns trimmed were collected at white, green and yellow anther stages (Fenton). Total RNA was prepared from each pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified CDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids These steps were performed in the TJ Close lab (Choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (UCI) (Begum, Panher, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see hitr://www.genome.
                                                                                                                                                                                              E Tobases I to 607)

S Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,

Wing,R., Close,J.J., Close,S.J., Oates,R. and Main,D.

Fenton,R.D., Close,S.J., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource
for barley genomics: Morex pre-anthesis spike cDNA library
Unpublished (2001)

On Jul 26, 2000 this sequence version replaced gi:13155022.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288
                                                                 Hordeum vulgare subsp. vulgare
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooldeae, Triticeae, Hordeum.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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sub_species="vulgare"
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High quality sequence stop: 585.
Location/Qualifiers
EST.
Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
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/lab host="DH10B"
/clone lib="AM1"
/clone lib="AM1"
/clone lib="AM1"
/note="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSport1; Site_1: Sal1; Site_2: Mot1; An unidirectional cDNA library generated from Rapical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 TrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLysLeuGluGluValArgLys
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Conservative:
Mismatches:
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                            ValHisileLeuGluAlaSerSerValProProLeuProGlu---AlaGlyGlyAsnAla 39
                                                                                                                                                                                                                                                                                                                          AlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSer 99
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 02
Seq primer: T7 Promoter Primer.
                                             ValGinargiysGlyAlaValAspProAspLysAspArgiysGluLysAlaAlaAla
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                                                                                                                                 Grcchalgeaagagccgrrcacccgaraaagaracaagaagaagaagaagcrcccga
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (Dases 1 to 665)
Vettore, A.L., da Silva, F.R., Kemper, E.L.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 uLeuValAsnLysIleArgAsnLysLys 167
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181 GlnAsnIleLysLeuArgAsn 187
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                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Spermatophyta, Spermatophyta, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="just_after the transition from vegetative to
inflorescence_development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAlaAlaAlaPro 60
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                                                                                                                                                Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548
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                                                                                                                                                                                                                              Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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Matches:
Conservative:
Mismatches:
Indels:
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Plate: 946064 row: A column: 10.
Location/Qualifiers
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                           GI:9733131
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575.50
76.47%
65.24%
                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                           Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@star
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           BE511883
BE511883.1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Gpermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 634)

S Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: pollen
Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
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/note="Organ: Pollen; Vector: pmE185-FL1; Site 1: XhoI;
/note="Organ: Pollen; Vector: pmE185 of from pollen at the late vacuolated archouse-grown panicles of sorghum line BTx623. Panicles were removed from the flag leaf prior to emergence, when no detectable amylase is present in pollen of male-fertile lines. This stage represents pollen collected from anthers about 8-14 days prior to anthesis, Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME1885-FL3 vector (5-prime DraIII site is CACTGTCTG, 3-prime DraIII site is CACTGTCTG,
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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Vutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. University of Tokyo Institute of Medical
Science, plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sugs (CTTCTGCTCTAAAAGCTGCG).
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291 ACTCTTATTGGTCAAGAGTTTGATGAGAAGAATATCAGGAGAGAGGAGTGTATGATGCTTTT 350
                                                                                                                               468 ATCAGGATTAAGAACAAGAAAAACTTCTCCAGGAAATTGAAAGACAGCTTGATGACTC
                                                                               AsnValLeuIleAlaLeuArgValIleAlaLysGluLysLysGluIleArgTrpMetGly
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POLI_25_C08_91_A002 Pollen Sorghum bicolor cDNA clone
POLI_25_C08_A002 5', mRNA sequence.
CP484481
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/clone="SCAGFL8013C10"
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(10cm-long); Vector: pSport1; Site 1: Sal1; Site 2: Not1;
An unidirectional CDNA library generated from [Developing inflorescence and rachis (10cm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 013 row: C column: 10
Seq primer: 77 Promoter Primer.
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23
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                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:4547"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AlaAlaAlaProArgileThrGlyTrpGlyLeuArgGluTyrSerLysileValCysGlu 76
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Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                                                                                                                                                     21 ValHisileLeuGluAlaSerSerValProProLeuPro----
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS81ZA03 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                     GlyAsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLys
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 ENRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachrer V., Weissenbach J., Salanoubat M.

WRGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : 5 prime and 3 frime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLGS7ZA12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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                                           542
                                                                                                                                                                     SerAsnTyrArgTyrGluLysIleLysLysLeuGluGluValArgLysGluLeuValAsn 161
                      ValleuileAlaLeuArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cng.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                      660 CAAAATATAAGTTCCGCAAC 679
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2 (bases 1 to 1403)
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1006 230 946

171 826

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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein http://www.genoscope.cns.ff/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubar, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                  06-FEB-2004
                                                    CNSO9ZIR

Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTLS73ZB01 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                          192 SerSerAlaGluAsnValAsn---GlyIleArgLeuPro-PheValLeuValLysThrSe 210
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(bases 1 to 1568)
                                                                                                                                               210 rArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGluPh
                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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/tissue type="Adult vegetative
/plasmid="pCMVSPORT_6"
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HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
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/strain="Col-0"
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                                   Direct Submission

Ly Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr - The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraise construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V. Aury J.M., Jaillan O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Wunich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 GGTGATGATGCTGCTTCTCAAGGAGCTTCTGGTGTTAAGAAGAAGAAGAAGAGGGGACAGCGT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 LeuLysSerMetAlaHisIleGly------GlnGlyPheAspGluLysAsn 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 ileArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValileAlaLys 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 GlulyslysglulleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLyslleLysLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLysLysAlaLeuLeuGln 171
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Matches:
Conservative:
Mismatches:
Indels:

    1418
    organism="Arabidopsis thaliana"

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/strain="Col-0"
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                   AUTHORS
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CK278661 592 bp mRNA linear EST 03-AUG-2004 EST724739 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAE738 5' end, mRNA sequence.
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Solanum tuberosum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, lamides, Solanales, Solanaceae, Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 MetalaHisIleGlyGlnGlyPheAspGluLysAsnIleArgArgArgValTyrAspAla 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 GlyLeuSerAsnTyrArgTyrGluLysileLysLysLeuGluGluValArg-LysGluLe 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 TTCAT-GTGCTCATTGCAATTCGTGTTATTGCAAAAGATAAAAAGGATATAAAGGATG
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151 ATTACGCAGAACGGTCTGGAGTTTGATGAGAAGAATATTAGGCGGAGGGTATATGATGCT
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1111
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Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cdna est clone
Web site: http://www.ncgr.ac.cn.
Location/Qualifiers
ce 1. .70
/ organism="Oryza sativa"
/ mol_type="mRNA"
/ db xref="kaxon:4530"
/ clone="p730d01p5"
/ clone="lib="Oryza sativa library (Ha
                                                                                                                                                                                                                                                                                                    Conservative:
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E thian-toideae; Oryzeae; Oryza.

E than, B., Feng, O., Huang, Y.C., Ying, K., Li, Y., Guan, J.P., Zhu, J.J., Meng, Q.J., Zhang, Y.L., Mu, Y.L., Mu, Z., Chen, L., Fan, D.L., Meng, Q.J., Lu, Y., Li, Y., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Yu, S.J., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, Chen, W., Wu, S.A. and Xue, Y.B.

Rice cDnA EST clone
Unpublished (2003)
Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, China
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clone
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                                                                                                                                                                                                                                                                                                          97 LeuLysSerMetAlaHisIleGly------GlnGlyPheAspGluLysAsn 111
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|TTAAAGAACGAACGACTCTCACTTAGGAACAGAATTGAGAAGAAAACTGCATATTCCCAA
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B) Oryza sativa cDNA
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P730d01p5, mRNA sequence.
CR286882
         Gaps:
                                            US-10-088-830-2 (1-261) x CNS09ZIR (1-1568)
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79 9 66 210 139 269 449

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Submitted (25-APR.2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.itgr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTC 16-OCT-2002
413 AAGAAAGCAGCCTATTTAGAAGAACTTGAAGATCAATATGTAGGGCTTCAAAACCTCATA 472
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                                                                            145 ArgTyrGluLysileLysLysLeuGluGluValArgLysGluLeuValAsnLysileArg 164
                                                                                                                                                                               165 AsnlyslysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLys 184
                                                                                                                                                                                                                                                                                                                             473 AAACGCAATGATCAGTTGTATGGCTCAGGCAATGCTCCTAGTGGTGGTGTGGCTTTACCG 532
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    (Dases 1 to 1245)

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                                                                                                                           353 GATGCAAATGATATTGAGGAGCTAAAGACTGAGCGTCTTAACTTGAGAATAGGATTGAA
                                                                                                                                                                                                                                                                                                                                                                                                            185 LeuArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeuPro
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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/db_xref="MaizeDB:634768"
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2 (bases 1 to 1245)
Coe, E.H.
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//Lab host="DH10B-TOTA"
//Lab host="DH10B-TOTA"
//Lab host="DH10B-TOTA"
//Lab host="DH10B-TOTA"
//Lab host="Vector: pCWNSport6.1; Site=1: BCSRI; Site=2: Not1;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mm Nacl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, dd, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought: stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4113"
/clone="POAE738"
/tissue_type="abiotic stress treated leaf and root tissue"
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                                                                                                                                                                          Bmail: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Other ESTs: EST724740
Cohtact: Robin Buell
The Institute for Genomic Research
                                                                                                                                                  9712 Medical Center Dr, Rockville, MD 20850, USA
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/cultivar="Kennebec"
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ArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGlu 132
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                                                                                                                                                                                                                                                                                  83 ArgThrThrTyrAsnGluValAlaAspGluIleTyrSerGluLeuLysSerMetAlaHis 102
                                                                                                                                                                                                                                                                                                                           -----IleGlyGlnGlyPheAspGluLysAsnIle 112
                                                                                                                                                                                                                                                                                                                                         247 AATATTGAGGCACCAGATCCTGATAACCCTAACGCGCAACAATATGATGAGAAAAAAATAT 306
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TCATATGGTTCAGGAAACACGCCTTCTGGTGGAGTGGCTTTGCCATTTATCCTAGTTCAG 597
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                                                                                                                                                                                             -----AlaValAspProAspLysAspArgLysLysGluLysAlaAlaAlaProArgIle 62
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                                                                                                                              CGAGGGGACAGCATCCTCCGCTTGAATAATCTCGACATCAACGGC------
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           Length:
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Search completed: February 7, 2005, 00:20:47 Job time : 3518 secs

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Sequence 465, App Sequence 12049, Sequence 120499, Sequence 15091, A Sequence 14679, A Sequence 16747, Sequence 576, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli

4380, Ap 13, Appl

Sequence Sequence Sequence

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Total number

Searched:

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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US-09-640-211A-465
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-4380
US-08-139-937-13
US-09-023-655-1230
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US-08-306-691B-18
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: PALO ALTO
CITY: PALO ALTO
COUTRY: USA
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US-09-517-584A-3
US-09-315-113-2
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US-08-481-814A-1
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INPORMATION:
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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US-09-023-655-1456
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  RESULT
    -MODEL=frame+_p2n.model -DEV=x1h
-Q=CQR01_1/USPTO gapol/USD1088830/runat 04022005_122603_29577/app_query.fasta_1.455
-Q=CQR01_1/USPTO gapol/USD1088830/runat_04022005_122603_29577/app_query.fasta_1.455
-LGOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR SCORE==pct -THR MAX=100 -THR MINEO -ALIGN=15
-UODELCOAL -OUTFMT=pto -NOFM=ext -HEAPSIZE=500 -MINIEN=0 -MAXEN=20000000
-USRR=US10088830_@CGN 1_1_69_@runat_04022005_122603_29577 -NCPU=6 -ICPU=3
-NO MAAP -LARGRQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-LONGLOG -LONGRANT -DSPBLOCK=100 -LONGLOG
-FGAPOP=6 -FGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
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Sequence 7,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                              - nucleic search, using frame_plus_p2n model
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US-09-10-861-5
US-09-123-415B-7
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US-09-189-627A-1
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Match
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Database :

Result

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918 ATGTCGTTTGGCCTGGAGTCAGGCAAATGCTCTCTG 953
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LOCATION: 1...
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 GluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArg 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 LysSer------MetAlaHislleGlyGlnGlyPheAspGluLysAsnIleArg 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 AlaGluAsnVal------AsnGlyIleArgLeuProPheValLeuValLysThr 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 SerArgiysAlaArgValGluIleGluIleSerAspAspSeriysPheAlaHis---Phe 228
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                               3.43e-39
399.50
58.33%
37.30%
          TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 14;
SEQUENCE CHARACTERISTICS:
LENGTH: 2320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: GENEBANK
(650) 855-0555
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                          CLONE: 9604478
US-09-023-655-1456
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                                                                                   APPLICANT: LaThargue, Nicholas B.
APPLICANT: LaThargue, Nicholas B.
APPLICANT: delaluna, Susana
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                           STATE: ALLIOU NO. 5859199CH G16DE KG. BER LIDOR COUTRY: USA
ZIP: AZ201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: 180PY disk
COMPUTER: IBM PC compatible
COMPUTER: BACCOMPACIBLE
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-5EP-1996
CIASSIFICATION DATA:
APPLICATION NUMBER: GB 9610195.1
REDIEFRATION NUMBER: CF ATHUR NUMBER: CTAMACOMPACIAL ATTHUR CAMACOMPACIAL ATTHUR NUMBER: 117-220
REFERRINGE/DOCKET NUMBER: 117-220
TELEFRAX: 703-816-4100
TELEFRAX: 703-816-4100
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; Sequence 5, Application US/08723415B; Patent No. 5859199; GENERAL INFORMATION:
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249 ArgAsnSerIleGlyArgAlaGlyArgAlaThrLeu 260
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Patent No. 6387649
GENERAL INFORMATION:
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                                                                                                                                                                                                                    174 GluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSer 193
                                              114 ArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLys
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                                 LysSer-------MetAlaHisIleGlyGlnGlyPheAspGluLysAsnIleArg
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CURRENT APPLICATION NUMBER: US/09/189, 627A
CURRENT FILING DATE: 1998-11-10
FRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
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Matches:
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Mismatches:
Indels:
Gaps:
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Patent No. 6159691
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APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
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389.50
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Best Local Similarity:
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ORGANISM: mouse
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SEQ ID NO 5
LENGTH: 1157
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18 LeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
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APPLICANT: La Thangue, Nicholas
APPLICANT: La Thangue, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REPERBNCE: 620-54
CURRENT APPLICATION NUMBER: U8/09/110,861
CURRENT PALLICATION NUMBER: U8/09/110,861
PRIOR PILING DATE: 1998-11-10
PRIOR PILING DATE: 1996-30
PRIOR FILING DATE: 1996-30
PRIOR FILING DATE: 1996-03-30
PRIOR FILING DATE: 1996-03-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
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496 CTCCTTCAGCAAATTGCTTTTAAAAACCTGGTACAGAGAAAATGGACAAAATGAACAA 555
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389.50
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                                                                   NAME/KEY: CDS
LOCATION: (1)..(1110)
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Best Local Similarity:
                            TYPE: DNA
ORGANISM: mouse
                                                                                                                             Alignment Scores
SEQ ID NO 5
LENGTH: 1157
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118 GTTCCCAGTGATAGAAACGAGCTAGAGAATTTATAGACTCTGATTTTTCAGAAAGTAAA 177
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Sequence 7, Application US/08723415B

Patent No. 5859199

GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: ALINGRON
STATE: VA
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ZIP: 22201-4741

COUNTRY READABLE FORM:
MEDIUW TYPE: FILPOPPY disk
COMPUTER READABLE FORM:
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: GB 9610195.1
PILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTAMFORM, Arthur R.
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEFRAK: 703-816-4100
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Mismatches:
Indels:
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389.00
57.48%
38.58%
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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Pred. No.:
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US-08-723-415B-7
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RESULT 5 US-08-723-415B-7

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GluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLys 151
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                                  IleArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys
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APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189, 627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR PLING DATE: 1996-09-30
PRIOR PLING DATE: 1996-05-15
PRIOR PRIOR FILING DATE: 25
SOFTWARE: PALENTIN VOS: 2.0
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US-09-189-627A-7
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ORGANISM: mouse
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LA THANGUE, NICHOLAB

APPLICANT: LA THANGUE, NICHOLAB

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REFERENCE: 620-54

CURRENT FILING DATE: 2000-11-13

PRIOR PRILICATION NUMBER: US/09/189,627

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

SEQ ID NOS: 25

SOFTWARE: PATENTIN VUMBER: 02

SEQ ID NO 7

LENGTH: 1202

LENGTH: 1202

TYPE: DNA

ORGANISM: mouse
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TGTGAGAAAGTTCAGCGGAAAGGCACAACTTCATACAATGAGGTAGCTGATGAGCTGGTA 294
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Conservative:
Mismatches:
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                                                                      Length:
                                                                                                                              Indels:
                                                                                                                                                                                                                     82 GTCACTCAGACTCACATAGCTGAGGCT---
                                                                   4.57e-38
389.00
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; NAME/KEY: CDS
; LOCATION: (1)..(1155)
US-09-710-861-7
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         TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                             CUDNIKK: U.S.

CUNTER SEADABLE FORM:
MEDIUM TYPE: Flopyy disk
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FLING DATE: 30-SEP-1996
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-ARY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REFERENCE/DOCKET NUMBER: 117-220
TELECHOMMINICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                3: NIXON & VANDERHYE P.C.
1100 No. 5859199th Glebe Rd.
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1385 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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57.48%
38.58%
29.49%
TITLE OF INVENTION: TRAIL TITLE OF INVENTION: THE NUMBER OF SEQUENCES: 21
CADDRESSEE: NIXON & VAN
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MOLECULE TYPE: cDNA
                                                                                                                                         CITY: Arlington STATE: VA
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Sequence 1, Application US/08723415B Patent No. 5859199 GENERAL INFORMATION: APPLICANT: LaThangue, Nicholas B

US-08-723-415B-1

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118 TGTGAGAAAGTTCAGCGGAAAGGCACAACTTCATACAATGAGGTAGCTGATGAGCTGGTA 477
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      301 GTTCCCAGTAGTAGAAAACGAGCTAGAGAATTTATAGACTCTGATTTTTCAGAAAGTAAA 360
                                                                                                                                                                                                                                                       478 rcrgAgrtTaccaacrcaartaaccarcrgGCAGCTGATTCGGCTTATGATCAGGAGAAC 537
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778 CAACAAAACCAGGCCCTCCAGCTGTGAATTCCACCATTCAGCTGCCATTTATAATCATT
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                                                                                                                                 CysGluLysValGluAlaLysGlyArgThrThrTyrAsnGluValAlaAspGluIleTyr
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                                             55 GluLysAlaAlaAlaProArgIleThrGlyTrpGlyLeuArgGluTyrSerLysIleVal
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TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILER REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/110,861
CURRENT FILING DATE: 2000-11-13
FRIOR APPLICATION NUMBER: US/09/189,627
FRIOR APPLICATION NUMBER: 08/723,415
FRIOR FILING DATE: 1998-11-10
FRIOR FILING DATE: 1996-09-30
FRIOR FILING DATE: 1996-05-15
FRIOR APPLICATION NUMBER: 08 9610195
FRIOR APPLICATION NUMBER: 08 9610195
FRIOR FILING DATE: 1996-05-15
SOFWARE: PARCHING DATE: 1996-05-15
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Patent No. 6387649
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
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; LOCATION: (1)..(1338)
US-09-710-861-1
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                                                                                                        GAAAAAAAAGAAATCAAGTGGATTGGCCTGCCTACCAATTCTGCTCAGGAATGCCAGAAC 657
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                                                                   GlulyslysGluileArgTrpMetGlyLeuSerAsnTyrArgTyrGlulysileLysLys 151
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CURRENT APPLICATION NUMBER: US/09/189, 627A
CURRENT FILING DATE: 1996-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SSOFTWARE: PATENTIN VEY: 2.0
SSOFTWARE: PATENTIN VEY: 2.0
LENGTH: 1385
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GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas APPLICANT: de la Luna, Susana
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Best Local Similarity:
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ORGANISM: mouse
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LOCATION: (1)
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US-09-189-627A-1
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RESULT 11
US-09-949-016-3349
; Sequence 3149, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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Mismatches:
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          Length:
Matches:
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Best Local Similarity:
Alignment Scores:
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Mismatches:
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       PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
SOFTWARE: FastSEO for Windows Version 4.0
SEQ ID NO 3349
TYPE: DNA
2000-04-14
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38.66%
29.19%
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                                                                                                                                                             ORGANISM: Human
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                             115 ArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLysGluLysLys
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; Sequence 3, Application US/09189627A
; Patent No. 6159691
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; TITLE OF INVENTION: TRANSCRIPTION PACTOR DP-3 AND ISOFORMS THEREOF
; CURRENT APPLICATION NUMBER: US/09/189,627A
; CURRENT FILING DATE: 1998-11-10
; PRIOR FILING DATE: 1996-09-10
; PRIOR FILING DATE: 1996-09-10
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; FROM 1993
; FROM 1993
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Best Local Similarity:
Query Match:
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ORGANISM: mouse
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LOCATION: (1)
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US-09-189-627A-3
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Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: detalluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
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Mismatches:
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Gaps:
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Matches:
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APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIPECATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPAN: 703-816-4100
TELEPAN: 703-816-4100
TELEPAN: 103-816-4100
TELEPAN: 115-816-4100
TELEPAN: 115-810-4100
TELEPAN: 115-810-4100
TELEPAN: 115-810-4100
TELEPAN: 115-810-41
                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd.
CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIF: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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Query Match:
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; LOCATION: 1..1
US-08-723-415B-3
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                                                         AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla 57
LeuThrGlyValHisileLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

GENERAL INFORMATION:

FACENTE INFORMATION:

APPLICANT: La Thangue, Nicholas

APPLICANT: La Thangue, Nicholas

APPLICANT: La THANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

FILE REFERENCE: 620-80-11-13

FILE REFERENCE: 620-11-13

FRICK APPLICATION NUMBER: US/09/710,861

CURRENT FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: 08/723,415

FRICK FILING DATE: 1996-09-30

PRIOR APPLICATION NUMBER: GB 9610195

PRIOR APPLICATION NUMBER: GB 9610195

PRIOR APPLICATION NUMBER: GB 9610195

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTING DATE: 1996-05-15

NUMBER: PATENTING DATE: 1996-05-15

SOFTWARE: PATENTING DATE: 1996-05-15

SOFTWARE: PATENTING DATE: 1996-05-15

SOFTWARE: PATENTING DATE: 1996-05-15

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                  GTCACTCAGACTCACATAGCTGAGGCTGCT-
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                                                                                                                                                                                                                                                                                                                                         38 AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                1.78e-37
384.00
57.37$
37.45$
                                                    (1)..(1107)
                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
ORGANISM: mouse
FEATURE:
                                 ; NAME/KEY: CDS
; LOCATION: (1)
US-09-710-861-3
                                                                                                         Alignment Scores:
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US-08-428-131-1
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126 LeuArgValileAlaLysGluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArg 145
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                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPRAIN SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PRENEUT Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,131

FILING DATE: 33-UW-1995

CLASSIFICATION: 514

ATTORNEY/ABCHT INFORMATION:

NAME: Arthur R. Crawford

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-181

TELEPHONE: (703) 816-4000

ITELEPHONE: (703) 816-4100

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

**CNAME OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE 
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87
41
60
17
                       APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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378.50
62.44%
42.44%
28.70%
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TYPE: nucleic acid
STRANDEDNESS: double
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55..1284
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                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
GENERAL INFORMATION:
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; LOCATION:
US-08-428-131-1
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769 AGAAATGGCCAAGCTGAGGCGCGCGCGCCTCCCAACTCTGTCATCCAC 828
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                                                                                                                                         942
166 LysLysAlaLeuLeuGinGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeu 185
                                                                                                                                                                                     222 AspSerLysPheAlaHis---PheGluPheAsnGlyAlaProPheThrLeuHisAspAsp 240
                                                                                                                                                                                                       186 ArgAsnGlnThrLeuGluSerSerAlaGluAsnVal------AsnGlyIleArg
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Description

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Publication No. US20040123343A1

Sequence 33888, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: About Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bukharov, Andrey A.
APPLICANT: Bukharov, Plants and Uses Thereof for Plant Improvement
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 33888
                                                                           Sequence 4115, Ap
Sequence 1190, Ap
Sequence 2013, Ap
Sequence 2013, Ap
Sequence 1456, Ap
Sequence 1176, Ap
Sequence 10136, Ap
Sequence 20983, A
Sequence 20136, A
Sequence 211642, A
Sequence 211, Appl
Sequence 21, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 1357, Ap
Sequence 1357, Ap
Sequence 1357, Ap
Sequence 21, Appl
Sequence 21, Appl
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                                                      8 US-10-437-963-33888

US-10-425-115-4115

US-10-425-114-4049

US-10-425-114-4049

US-10-425-115-8731

US-10-425-115-8731

US-10-425-115-8731

US-10-425-115-8731

US-10-954-456-1176

US-10-954-456-117643

US-10-954-456-117643

US-10-186-887-1357

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US-10-10-186-88-569

US-10-424-59-4656

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US-10-425-114-2051

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US-10-085-783A-27279
US-10-856-499-576
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Result
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-MODEL=frame+ p2n.model -DEV=xlh
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-NATEN=2000000000 -USER=S310088830_@CGN 1 1.480_@runat_04022005_122604_29641
-NCPUSE -ICPUS=3 -NO MMAP -LARGEQUERY -NGG $CORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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                                                                                                             February 6, 2005, 23:22:07; Search time 580 Seconds (without alignments) 2590.084 Million cell updates/sec
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1 MAPPRGGAAAAATAALDLTG.....SILEGVRRNSIGRAGRATLH
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Listing first 45 summaries
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Potal number of

Searched:

Perfect score:

Sequence:

protein

Run on:

Scoring table:

SUMMARIES

Sequence 36537, A Sequence 64593, A Sequence 23, Appl Sequence 23, Appl Sequence 266, App Sequence 465, App Sequence 9935, Ap Sequence 91931, A Sequence 98311, A

Sequence 1294, Ap Sequence 1294, Ap Sequence 440, App Sequence 12, App] ~

516 209 456 229 249

336

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APPLICANT: IN CACALLOW:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Avoid M.
APPLICANT: APPLICANT: Avoid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(5)222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 4115
LENGTH: 774
                                                                                                                                                                                 LeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThr 189
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                                                                              190 LeuGluSerSerAlaGluAsnValAsnGlyIleArgLeuProPheValLeuValLysThr
                                                                                                                                                            SerArgLysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHisPheGlu
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Matches:
Conservative:
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; OTHER INFORMATION: Clone ID: MRT4577_103754C.1
US-10-425-115-4115
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-425-115-4115
Sequence 4115, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 995 TACCCCGGCGGTAAGCCCGGTAACCGCGGTAACCGCGCGCTTACCGGCGGTATGGTGAAC 936
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              TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity:
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LENGTH: 1406
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Sequence 409, Application US/10425114
; Sequence 409, Application US/200400348881
; Publication No. US200400348881
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Screen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (5313) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4049
; LENGTH: 1350
                                                                                                                                                                                                                                                                                                                                                                                 1008 CCTCACGCAACAGTAGAAGTGGAGATATCAGAAGATATGCAGCTCGTGCATTTTGATTTC 1067
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                                                                                                                                                                                                                                                                                             172 GluIleGluLygGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGlu 191
                                                                                                                                                      132 GluLysLysGluIleArgTrpMetGlyLeuSerAsnTyrArgTyrGluLysIleLysLys 151
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                                                                                                           192 SerSerAlaGluAsnValAsn---GlylleArgLeuProPheValLeuValLysThrSer
                     GlnGlyPheAspGluLysAsn
                                                                                       112 ileArgArgArgValTyrAspAlaPheAsnValLeuIleAlaLeuArgValIleAlaLys
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Matches:
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ORGANISM: Zea mays
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SQUENCE 1190, Application US/10739930

SQUENCE 1190, Application US/10739930

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REPERBUCE: 38-21 [53377]

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

SEQ ID NO 1190

LENGTH: 1639
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                                                                                     LeuSerAsnTyrArgTyrGluLysIleLysLeuGluGluValArgLysGluLeuVal 160
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                                                                                                                                                                                                                                                                                                                                             eArgLeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSe
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101 AlaHisIleGlyGlnGlyPheAspGluLysAsnIleArgArgArgValTyrAspAlaPhe
                                                                                                                                                                                                                             168 GGTGATGATGCTGGTTCTCAAGAGCTTCTGGTGTTAAGAAGAAGAAGAAGAAGAAGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pleuSerileleuGluGlyValArgArgAsnSerileGlyArgAla 255
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US-10-739-930-1190
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US-10-425-115-87351
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Fublication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LA Rosa, Thomas J.
APPLICANT: APPLICANT: David K.
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: Anou, Yihua
APPLICANT: APPLICANT: Anou, Yihua
APPLICANT: APPLICANT: Anou, Yihua
APPLICANT: APPLICANT: Anou, Yihua
APPLICANT: APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
                                                                                                                                                                                                 264 ATGAGAGTATCTGAGAAAGTCGAAAGGAGAAAACGAGAAACCTACAATGAGGTGGCAGAC 323
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                                                                                    SerAspAspSerLysPheAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAsp
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; OTHER INFORMATION: Clone ID: MRT4577_101857C.1
US-10-425-115-2033
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ORGANISM: Zea mays
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677 CAAAACTIGGITCGGCGAAAIGAGCAGCTAIAIGGGTCAGGAGAIGCACCTICCGGIGGA
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797 TCAGAAGATATGCAGCACGTGCATTTTGATTTCAATAGCACTCCATTTGAGTTGCAGGAT
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Mismatches:
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Gaps:
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; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
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APPLICANT: Language J
APPLICANT: Kovalic David K
APPLICANT: Shou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
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              598 ACCCGACCTCATGCTACCGTGGAAGTTGAGATATCAGAAGATATGCAGCTGGTGCATTTT 657
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                                                                                                                       658 GACTTCAATAGCACCCCATTCGAGCTGCACGACGACTCATACGTCCTAAAAGAAATGCGA
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Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules i
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53122) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
ENGTH: 1585
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Best Local Similarity:
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Sequence 1176, Application US/09954456
Batent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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267 GATAGAAAACGGGCTAGAAATTTATAGACTCTGATTTTTCAGAAAGTAAACGAAGCAAA 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 ATAGAGAAGCAGAGGGGGATAGAACGGATAAAGCAGAAGGGGCCCAGCTGCAAGAACTT
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                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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399.50
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Best Local Similarity:
      JS-10-641-643-1456
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                                                 Alignment Scores:
Pred. No.:
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                                                                              566 AATGATATTGAAGAACTAAAGACAGAGCGGCTTGGGCTCAGGAATAGAATTGAAAAGAAA 625
                                                                                                                                                                             685
                                                                                                                                                                                                               gAsnGlnThrLeuGluSerSerAlaGluAsnValAsnGly---IleArgLeuProPheVa 205
                                                                                                                                                                                                                                            ||||||||:::|||
-TTGGTACAGACACGCCCTCATGCAACTGGGGGAATGAAATATCAGAAGATATGCAGCT 804
                                                                                                                                                                                                                                                                                                                                                                                     225 eAlaHisPheGluPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerlleLeuGl 245
                                                                                                                                                                                                                                                                                                                                                                                                              805 TGTTCATTTTCATTTCAATAGCACTCCTTTTGAGCTGCATGATCATTATGTTCTCAA 864
506 GATATTATTTCCAAGGACAAAAAGGAAATTCAATGGAGGGGCCTTCCTCGTACTACTGTG 565
                                      147 GluLysIleLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsnLys
                                                                                                                           LysAlaLeuLeuGlnGluIleGlu-LysGlnPheAspAspleuGlnAsnIleLysLeuAr
                                                                                                                                                                                                                                                                                                205 lieuvaliysThrSerArgiysAlaArgValGluileGluileSerAspAspSerLysPh
                                                                                                                                                  626 ACAGCCIATCIGCAGGAGCTIGAGGAGCAATICATAGGTCTTCAGAACCTTATTCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SNT APPLICATION DATA:
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/641,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITION FOR GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1455, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Sellhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (650) 855-0555
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INFORMATION FOR SEQ ID NO: 1456:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2320 base pairs
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: singl
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COMPUTER READABLE FORM:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCAATGAAA 874
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APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
ITILE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: HUMAN PROSTATE CANCER
ITILE OF INVENTION: HUMAN PROSTATE CANCER
ITILE OF INVENTION: HUMAN PROSTATE CANCER
ITILE OF INVENTION: HUMAN PROSTATE CANCER
INITILE OF INVENTION: HUMAN PROSTATE CANCER
ITILE OF INVENTION: MINDER: 00/105,204
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2000-02-17
PRIOR PAPLICATION NUMBER: 60/103,39
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-12-13
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR PRIOR APPLICATION NUMBER: 60/255,281
PRIOR PRIOR APPLICATION NUMBER: 60/255,281
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PRIOR APPLICATION NUMBER: 60/255,281
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                              18 LeuThrGlyValHigileLeuGluAlaSerSerValProProLeuProGluAlaGlyGly 37
                                                                                                                                                                                                               195 GluAsnVal------AsnGlyIleArgLeuProPheValLeuValLysThrSer
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-357-930-20983
Sequence 20983, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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219 AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA 275
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CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
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| AGAAAAACAGTCATAGATTGCAGCATCTCCAGTGAC---AAGTTTGAGTATCTTTTCAAT 894
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                                                                                       AlaAlaProArglleThrGlyTrpGlyLeuArgGluTyrSerLyslleValCysGluLys 77
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AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla
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Mismatches:
Indels:
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PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26827
LENGTH: 2968
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yinua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

VURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 1/642

LENGTH: 476
                                                                                                                                     229 uPheAsnGlyAlaProPheThrLeuHisAspAspLeuSerIleLeuGluGlyValArgAr 249
                                                                                                                                                                                                                                                                                           558 AGAGAAGCAGAGGGGGATAGAACGGATAAAGCAGAAGGGGGCCCAGCTGCAAGAACTTCT 717
                                       174 uLysGlnPheAspAspLeuGlnAsnIleLysLeuArgAsnGlnThrLeuGluSerSerAl 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 uleuValAsnLysIleArgAsnLysLysAlaLeuLeuGlnGluIleGluLysGlnPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 GATTICAGAGAACTCAAAGTITGCTGGTTTCGACTICAACTGTACACCATTCACCTTGCA
                                                                           718 CCTACAGCAAATGGCTTTCAAAAACCTGGTACAGAGAAATGGACAAAATGAGCAGGAAAA
                                                                                                               194 aGluAsnVal------AsnGlyIleArgLeuProPheValLeuValLysThrSe
                                                                                                                                                                                          rArgiysAlaArgValGluIleGluIleSerAspAspSerLysPheAlaHis---PheGl
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Indels:
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Matches:
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Publication No. US20040172684A1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGGAGATAAA---AATGGGAAAGGCTTGAGACACTTTTCAATGAAAGTGTGTGAGAAA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LysSerMetalaHisIleGly-----GlnGly-PheAspGluLysAsnIleArgAr 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAATICAAATAACCATITGGCTGCTGATICGGGCTTATGATCAGAAGAACATIAGGCG 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AsnAlaValGlnArgLysGlyAlaValAspProAspLysAspArgLysLysGluLysAla 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 LeuThrGlyValHisIleLeuGluAlaSerSerValProProLeuProGluAlaGlyGly
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PELING DATE: 2002-07-18
PRIOR FILING DATE: 2001-07-18
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GTTACTCAGACACACATAGCAGAAAGCTACTGGGTCCCT
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Mismatches:
Indels:
                       250 AsnSerIleGlyArgAlaGlyArgAlaThrLeu
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10136
LENGTH: 2968
                                                                                                         Sequence 10136, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
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US-10-198-846-10136
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387.00
58.33
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29.34
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    146 TyrGluLysIleLysLysLeuGluGluValArgLysGluLeuValAsnLysIleArgAsn
                       838 CTAAGCGATATTGAAGAGCTAAAGTCAGAGCGTCTTGGGCTCAGGAATAGAATTGAAAAG
                                                                   LysLysAlaLeuLeuGlnGluIleGluLysGlnPheAspAspLeuGlnAsnIleLysLeu
                                                                                 186 ArgAsnGlnThrLeuGluSerSerAlaGluAsnValAsn---GlyIleArgLeuProPhe
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/10206901B
Publication No. US20030100540A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ZHANG, ZHONGHUA
APPLICANT: ZHANG, ZHONGHUA
APPLICANT: DUBOIS, RAYMOND
TITLE OF INVENTION: IDENTIPICATION OF NSAID-REGULATED GENES
TILE REFERENCE: VBLT:0120S
CURRENT APPLICATION NUMBER: US/10/206,901B
PRIOR APPLICATION NUMBER: 60/308,370
PRIOR FILING DATE: 20001-07-27
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 692
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Best Local Similarity:
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ORGANISM: Homo
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Pred. No.:
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                                                                                     Sequence 43105, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Kovala Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tyrserlys1leValCysGluLysValGluAlaLysGlyArgThrTyrAsnGluVal
                  300 TGACGATGTCTCAATCCTTGAAGCGATCAGGTGTAATAAT 339
sAspAspLeuSerIleLeuGluGlyValArgArgAsnSer 251
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96
40
63
86
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US-10-424-599-43105
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Mismatches:
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47.89%
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                              277 ATGAACATCTCCCAAGGAGAAGAGAGATCAAGTGGATTGGTCTGCCCACCAACTCG 336
                                                                           186 ArgAsnGlnThrLeuGluSerSerAlaGluAsnVal-------AsnGlyIleArg 201
                                                                                                       202 LeuProPheValLeuValLysThrSerArgLysAlaArgValGluIleGluIleSerAsp 221
                                                                                                                                                               241 LeuSerIleLeuGlu 245
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